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OM nucleic - nucleic search, using sw model

Run on: May 12, 2005, 18:13:14 ; Search time 1223 Seconds
(without alignments)
17638.215 Million cell updates/sec

Title: PCT-US03-32302-1
Perfect score: 3644
Sequence: 1 atgagagtattatttgatga.....acccatgcggaatccactag 3644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3644	100.0	3644	12	ADN36593	Adn36593 Human pro
	2	2719.8	74.6	3912	12	ADJ96570	Adj96570 Human Nim
	3	2656.6	72.9	3919	10	AAD59965	Aad59965 Human 148
	4	2656.6	72.9	3919	12	ADQ15169	Adq15169 Human can
	5	2299.2	63.1	2562	5	AAH77990	Aah77990 Partial n
	6	2299.2	63.1	2562	12	ADN36597	Adn36597 Human pro
	7	1708.2	46.9	2043	12	ADN36598	Adn36598 Human put
	8	1705	46.8	2043	10	ADA53800	Ada53800 Human cod
	9	1705	46.8	2043	12	ADN36599	Adn36599 Human cDN
	10	1305.2	35.8	2638	12	ADQ64826	Adq64826 Novel hum
	11	1266.8	34.8	1601	12	ADN36600	Adn36600 Human cDN
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	15	660	18.1	861	4	ABK43499	Abk43499 DNA encod
	16	660	18.1	861	12	ADI53886	Adi53886 cDNA enco
	17	429.6	11.8	470	4	AAS27520	Aas27520 cDNA enco
	18	429.6	11.8	470	4	AAL01851	Aal01851 Human rep
	19	429.6	11.8	470	4	ABL97144	Abl97144 Human tes
	20	429.6	11.8	470	4	ABK43815	Abk43815 DNA encod
	21	429.6	11.8	470	10	ADB93698	Adb93698 Human cDN
	22	429.6	11.8	470	12	ADI54202	Adi54202 cDNA enco
	23	370.4	10.2	783	6	ABK52073	Abk52073 cDNA enco
	24	338	9.3	220860	12	ADN36595	Adn36595 Human pro
c	25	300.4	8.2	495	6	ABK52074	Abk52074 Human ser
	26	187.4	5.1	192	10	ADE85645	Ade85645 Farnesyl
	27	126.4	3.5	667	6	ABK52075	Abk52075 Human ser
	28	105	2.9	463	11	ACN81587	Acn81587 Breast ca
	29	104.8	2.9	400	4	AAL11386	Aal11386 Human bre
	30	101.2	2.8	415	4	AAL20285	Aal20285 Human bre
c	31	99.6	2.7	100	12	ADK42861	Adk42861 Biogeogra
	32	95.8	2.6	2249	6	AAD32675	Aad32675 Murine NE
	33	84	2.3	3714	13	ADR08309	Adr08309 Full leng
	34	79.8	2.2	1600	4	ABK43529	Abk43529 DNA encod
	35	79.8	2.2	1600	12	ADI53916	Adi53916 cDNA enco
	36	79	2.2	906	3	AAZ99725	Aaz99725 cDNA enco
	37	79	2.2	906	12	ADH16908	Adh16908 Human Nek
	38	79	2.2	3854	3	AAZ40661	Aaz40661 Human ser
	39	79	2.2	4087	4	AAH34880	Aah34880 Human col
	40	79	2.2	4087	4	AAF75335	Aaf75335 Human TGF
	41	79	2.2	4137	3	AAZ99724	Aaz99724 cDNA enco
	42	79	2.2	4240	5	ADL63811	Adl63811 Human ova
	43	76.2	2.1	939	12	ADH16906	Adh16906 Human Nek
	44	76.2	2.1	1346	3	AAZ40664	Aaz40664 Human ser
	45	76.2	2.1	1597	6	ABK52766	Abk52766 cDNA enco

ALIGNMENTS

RESULT 1
ADN36593
ID ADN36593 standard; DNA; 3644 BP.
XX
AC ADN36593;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human protein kinase HPK3P23 coding sequence.
XX
KW ds; gene; cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischemia; reperfusion.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .3051
FT /*tag= a
FT /product= "HPK3P23 protein"
FT /function= "protein kinase"
XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
DR P-PSDB; ADN36594.

XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Claim 2; SEQ ID NO 1; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,
CC preventing and treating kinase-related diseases, in particular, diseases
CC associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC autoimmune disorders, retinal detachment, stroke, epilepsy or
CC ischemia/reperfusion. This sequence corresponds to the coding sequence
CC for the HPK3P23 protein.
XX
SQ Sequence 3644 BP; 1117 A; 742 C; 851 G; 934 T; 0 U; 0 Other;

Query Match 100.0%; Score 3644; DB 12; Length 3644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60
Db    1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60

Qy   61 ATCTTGTTCCTTGCTTCCTTGGGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120
Db   61 ATCTTGTTCCTTGCTTCCTTGGGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120

Qy  121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180
Db  121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180

Qy  181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240
Db  181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240

Qy  241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300
Db  241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300

Qy  301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360
Db  301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360

Qy  361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420
Db  361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420

Qy  421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480
Db  421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480

Qy  481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540
Db  481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540

Qy  541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600
Db  541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600

Qy  601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660
Db  601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660

Qy  661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720
Db  661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720

Qy  721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780
Db  721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780

Qy  781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840
Db  781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840

Qy  841 GCAAAAAGTAATCTATTACAGGTAATAAACATGTCTCTTGTCCTTCAGTATCAAGTTATT 900
Db  841 GCAAAAAGTAATCTATTACAGGTAATAAACATGTCTCTTGTCCTTCAGTATCAAGTTATT 900

Qy  901 GAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGT 960
Db  901 GAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGT 960

Qy  961 GATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTG 1020
Db  961 GATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTG 1020

Qy 1021 AAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATA 1080
Db 1021 AAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATA 1080

Qy 1081 GGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTT 1140
Db 1081 GGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTT 1140

Qy 1141 AGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCA 1200
Db 1141 AGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCA 1200

Qy 1201 TTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACA 1260
Db 1201 TTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACA 1260

Qy 1261 ATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAA 1320
Db 1261 ATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAA 1320

Qy 1321 AATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTC 1380
Db 1321 AATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTC 1380

Qy 1381 AGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATA 1440
Db 1381 AGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATA 1440

Qy 1441 CAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTG 1500
Db 1441 CAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTG 1500

Qy 1501 ACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTG 1560
Db 1501 ACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTG 1560

Qy 1561 GCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCT 1620
Db 1561 GCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCT 1620

Qy 1621 TGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGC 1680
Db 1621 TGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGC 1680

Qy 1681 TGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCC 1740
Db 1681 TGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCC 1740

Qy 1741 TTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAA 1800
Db 1741 TTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAA 1800

Qy 1801 AAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATT 1860
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Db       1801 AAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATT 1860

Qy       1861 GTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACA 1920
Db       1861 GTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACA 1920

Qy       1921 TCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTT 1980
Db       1921 TCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTT 1980

Qy       1981 ATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAG 2040
Db       1981 ATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAG 2040

Qy       2041 ACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAA 2100
Db       2041 ACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAA 2100

Qy       2101 CTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAA 2160
Db       2101 CTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAA 2160

Qy       2161 GACAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAA 2220
Db       2161 GACAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAA 2220

Qy       2221 GATACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGT 2280
Db       2221 GATACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGT 2280

Qy       2281 TCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGA 2340
Db       2281 TCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGA 2340

Qy       2341 GGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCA 2400
Db       2341 GGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCA 2400

Qy       2401 GCTTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATT 2460
Db       2401 GCTTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATT 2460

Qy       2461 AAGGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATT 2520
Db       2461 AAGGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATT 2520

Qy       2521 CTTCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCA 2580
Db       2521 CTTCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCA 2580

Qy       2581 GGAATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTA 2640
Db       2581 GGAATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTA 2640

Qy       2641 ATTCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTG 2700
Db       2641 ATTCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTG 2700

Qy       2701 AAAAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGT 2760
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Db       2941 ATGCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAAC 3000

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Db       3001 AGGTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGC 3060

Qy       3061 ATTTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGC 3120
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Qy       3121 AAGATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGC 3180
Db       3121 AAGATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGC 3180

Qy       3181 CTGCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGG 3240
Db       3181 CTGCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGG 3240

Qy       3241 GCTTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAG 3300
Db       3241 GCTTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAG 3300

Qy       3301 AAAATGCTGCAAAATTCATCTTTTGGAGGATTGAGCATCGAATGGTATCTTCATTCTACA 3360
Db       3301 AAAATGCTGCAAAATTCATCTTTTGGAGGATTGAGCATCGAATGGTATCTTCATTCTACA 3360

Qy       3361 TTCGCTACGATGCGGCATCAACAAGGCGGGTGGGAGTTCGCATCACACCAGATCAAGGTG 3420
Db       3361 TTCGCTACGATGCGGCATCAACAAGGCGGGTGGGAGTTCGCATCACACCAGATCAAGGTG 3420

Qy       3421 GGGTCAGAATTCCAAAAAAAGATGTCACAGGAACTGGGGAGACCCCTAAAACAGTTGAGA 3480
Db       3421 GGGTCAGAATTCCAAAAAAAGATGTCACAGGAACTGGGGAGACCCCTAAAACAGTTGAGA 3480

Qy       3481 GACACCCAGGTGAAGAGTCCAAGTTTTGGACTGGATACGAAGATTTTGGAATTGCTAGTG 3540
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Qy       3541 CATTGGTGAGAGTAGACTCTAACAATGTGCATGAAAGTGGAAAGAAAGAGAAGACTCCAG 3600
Db       3541 CATTGGTGAGAGTAGACTCTAACAATGTGCATGAAAGTGGAAAGAAAGAGAAGACTCCAG 3600

Qy       3601 AAATAAGGGCCTATCCTGAAGAACACCCATGCGGAATCCACTAG 3644
Db       3601 AAATAAGGGCCTATCCTGAAGAACACCCATGCGGAATCCACTAG 3644
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RESULT 2
ADJ96570
ID ADJ96570 standard; DNA; 3912 BP.
XX
AC ADJ96570;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Nim-A related protein kinase NEK10 DNA SeqID 27.
XX
KW gene; ds; kinase; human; SNP; single nucleotide polymorphism;
KW tyrosine protein kinase; serine/threonine protein kinase; PTK; STK;
KW gene therapy; cancer; immune-related disease; cardiovascular disease;
KW brain; neuronal associated disease; metabolic; inflammatory disorder;
KW cytostatic; neuroprotective; immunomodulator; antiinflammatory;
KW Nim-A related protein kinase; NEK10.
XX
OS Homo sapiens.
OS 53.
XX
FH Key   Location/Qualifiers
FT variation   replace(1149,c)

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FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1849,a)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(2967,a)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
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PN   WO2004006838-A2.
XX
PD   22-JAN-2004.
XX
PF   15-JUL-2003; 2003WO-US021730.
XX
PR   15-JUL-2002; 2002US-0395632P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Whyte D,  Manning G,  Caenepeel S;
XX
DR   WPI; 2004-122753/12.
DR   P-PSDB; ADJ96636.
XX
PT   New nucleic acid molecule encoding a kinase polypeptide, useful for
PT   preparing a composition for treating diseases or disorders, e.g., cancer,
PT   or neurological, immunological or inflammatory disorders.
XX
PS   Example 1; SEQ ID NO 27; 366pp; English.
XX
CC   This invention relates to a novel isolated, enriched or purified nucleic
CC   acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC   to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC   as well as protein kinase-like enzymes. The present invention describes
CC   screening methods to identify agonists, antagonists and antibodies that
CC   can be used to modulate the activity or function of the mammalian kinase
CC   enzymes. As such, these compositions can be used for gene therapy
CC   purposes to treat diseases or disorders including cancer, immune-related
CC   diseases, cardiovascular disease, brain or neuronal associated disease,
CC   metabolic and inflammatory disorders. Accordingly, they exhibit
CC   cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC   activities. This polynucleotide sequence is a human kinase DNA sequence
CC   of the invention.
XX
SQ   Sequence 3912 BP; 1243 A; 784 C; 897 G; 988 T; 0 U; 0 Other;

  Query Match             74.6%;  Score 2719.8;  DB 12;  Length 3912;
  Best Local Similarity   91.4%;  Pred. No. 0;
  Matches 3031;  Conservative    0;  Mismatches   37;  Indels  249;  Gaps    4;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 721

Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 781

Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 841

Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        842 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 901

Qy        353 ------------------------------------------------------------ 352

Db        902 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 961

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 1021

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Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
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Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
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Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
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Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
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Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
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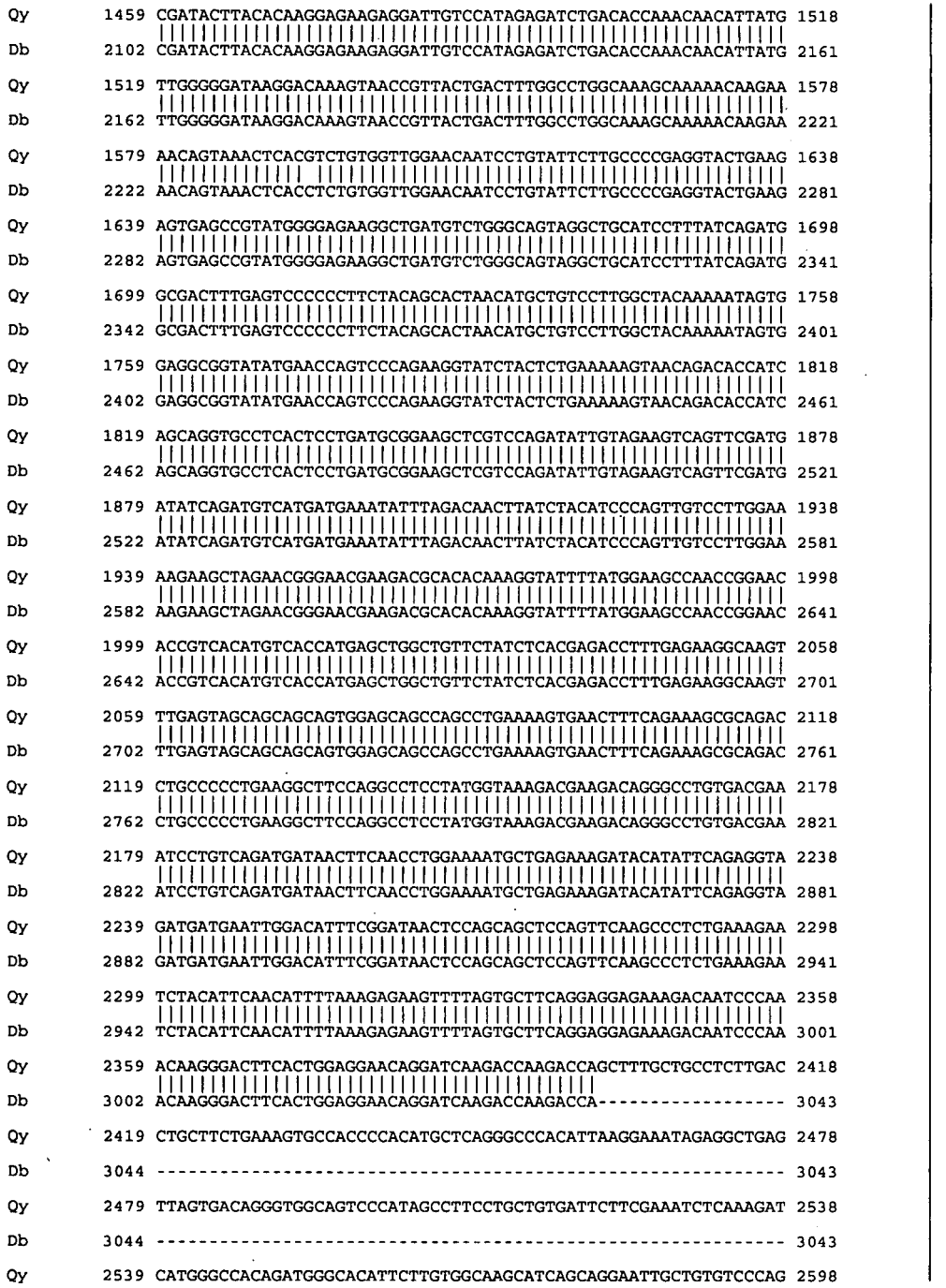
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RESULT 3
AAD59965
ID AAD59965 standard; cDNA; 3919 BP.
XX
AC AAD59965;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human 14815 cDNA.
XX
KW Human; 14815 protein; therapy; neurological disease; apoptotic disease;
KW metabolic disease; inflammatory disease; neuroprotective; cytostatic;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

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XX
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XX
PR   02-JAN-2002; 2002US-0345853P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers RE;
XX
DR   WPI; 2003-688693/65.
DR   P-PSDB; AAE39514.
XX
PT   New nucleic acid molecules, designated 14815 nucleic acids, useful for
PT   preparing a composition for diagnosing or treating neurological,
PT   inflammatory, apoptotic or metabolic diseases.
XX
PS   Claim 1; Page 40-44; 59pp; English.
XX
CC   The invention relates to novel 14815 protein, a member of kinase family
CC   and polynucleotide encoding such protein. Sequences of the invention are
CC   useful for detecting a molecule that binds to the polypeptide, including
CC   molecules that modulate their activity. They are useful in the diagnosis
CC   or treatment of neurological, inflammatory, apoptotic or metabolic
CC   diseases. The present sequence is human 14815 cDNA
XX
SQ   Sequence 3919 BP; 1253 A; 790 C; 895 G; 980 T; 0 U; 1 Other;

  Query Match             72.9%;  Score 2656.6;  DB 10;  Length 3919;
  Best Local Similarity   90.4%;  Pred. No. 0;
  Matches 2999;  Conservative    0;  Mismatches   39;  Indels  279;  Gaps    4;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
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Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
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Qy        353 ------------------------------------------------------------ 352

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Qy       2059 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2118
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Db       2709 TTGAGTAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2768

Qy       2119 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2178
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Db       2769 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2828

Qy       2179 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2238
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2419 CTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGGCTGAG 2478

Db       3050 ------------------------------------------------------------ 3049

Qy       2479 TTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCAAAGAT 2538

Db       3050 ------------------------------------------------------------ 3049

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Qy       2599 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2658
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Qy       3259 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3318
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Qy       3319 TCTTTTGGAGGATTGAG 3335
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RESULT 4
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DT   07-OCT-2004  (first entry)
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DE   Human cancer related gene, 14815.
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KW   Cancer; angiogenic disorder; cytostatic; antiangiogenic; gene therapy;
KW   human; gene; ds.
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XX
FH   Key             Location/Qualifiers
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PN   WO2004058153-A2.
XX
PD   15-JUL-2004.
XX
PF   16-DEC-2003; 2003WO-US040226.
XX
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PR 23-DEC-2002; 2002US-0436443P.
PR 07-JAN-2003; 2003US-0438498P.
PR 31-JAN-2003; 2003US-0444370P.
PR 06-FEB-2003; 2003US-0446031P.
PR 11-MAR-2003; 2003US-0453635P.
PR 25-MAR-2003; 2003US-0457199P.
PR 10-APR-2003; 2003US-0462458P.
PR 30-APR-2003; 2003US-0466732P.
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PR 03-JUN-2003; 2003US-0475472P.
PR 12-JUN-2003; 2003US-0478150P.
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PR 29-JUL-2003; 2003US-0490866P.
PR 02-SEP-2003; 2003US-0499614P.
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PR 06-NOV-2003; 2003US-0517742P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lightcap ES, Ecsedy JA, Hunter JJ, Macbeth KJ, Nestor MT;
XX
DR WPI; 2004-525772/50.
DR P-PSDB; ADQ15170.
XX
PT Identifying a compound capable of treating cancer or an angiogenic
PT disorder by combining a compound to be tested with e.g., 15986, 2179 or
PT 13249 polypeptide and detecting binding of the test compound to the
PT polypeptide.
XX
PS Claim 17; SEQ ID NO 127; 576pp; English.
XX
CC The invention relates to a novel method for identifying a compound
CC capable of treating cancer or an angiogenic disorder. The method
CC comprises: combining a compound to be tested with a cancer related
CC polypeptide; and detecting binding of the test compound to the
CC polypeptide. The invention further comprises: identifying a subject
CC having or at risk for developing cancer; and treating a subject having a
CC cancer or a cancer characterised by aberrant 15986, 2188, 20743, 9148,
CC 9151, 9791,44252, 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411,
CC 15088, 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694, 15701,
CC 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201, 6985, 9883, 12238,
CC 18057, 21617, 39228, 49928, 54476, 62113, 64316, 12264, 32362, 58198,
CC 2887, 3205, 8557, 9600, 9693, 44867, 53058, 55556, 57658, 2208, 10252,
CC 10302, 14218, 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827,
CC 21708, 3801, 64698, 2179 or 13249 cancer related polypeptide activity or
CC nucleic acid expression. The method and compounds have cytostatic and
CC antiangiogenic activities. The cancer related genes may be used in gene
CC therapy to treat disorders. The method is useful in identifying a
CC compound capable of treating cancer or an angiogenic disorder. This
CC polynucleotide sequence represents a human cancer related gene used in
CC the method of the invention.
XX
SQ Sequence 3919 BP; 1253 A; 790 C; 895 G; 980 T; 0 U; 1 Other;

Query Match 72.9%; Score 2656.6; DB 12; Length 3919;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 2999; Conservative 0; Mismatches 39; Indels 279; Gaps 4;

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Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
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Qy        353 ------------------------------------------------------------ 352

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Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
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Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
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Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
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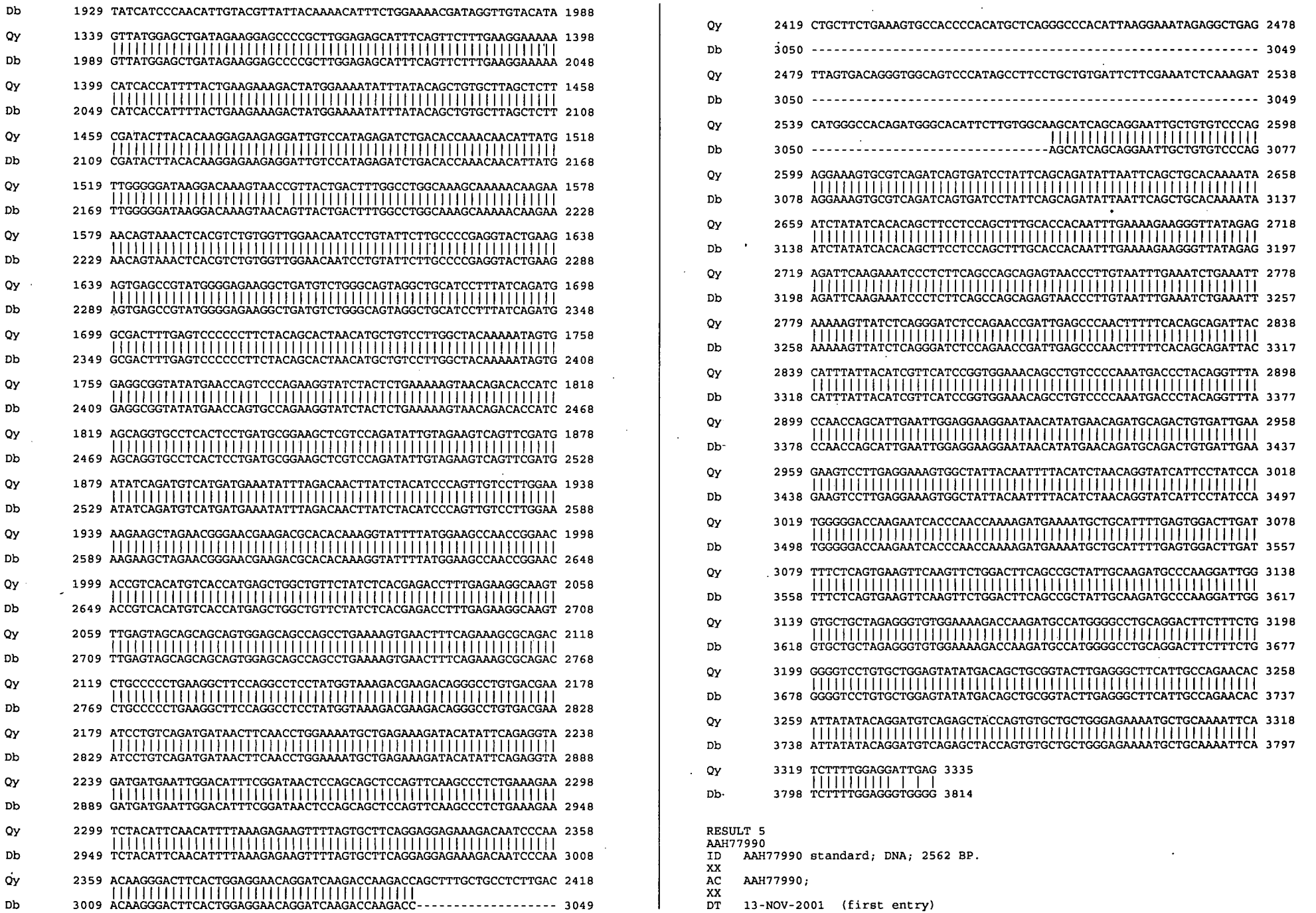
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RESULT 5
AAH77990
ID AAH77990 standard; DNA; 2562 BP.
XX
AC AAH77990;
XX
DT 13-NOV-2001 (first entry)

XX
DE Partial nucleotide sequence of human protein kinase SGK237.
XX
KW Human; protein kinase; cancer; immune disease; cardiovascular disease;
KW brain disease; neuronal disease; Alzheimer's disease; chromosome 3;
KW Parkinson's disease; multiple sclerosis; metabolic disorder;
KW peripheral nervous system disease; amyotrophic lateral sclerosis;
KW infection; ocular disease; migraine; pain; sexual dysfunction;
KW mood disorder; attention disorder; cognition disorder; hypotension;
KW hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN WO200166594-A2.
XX
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US006838.
XX
PR 06-MAR-2000; 2000US-0187150P.
PR 29-MAR-2000; 2000US-0193404P.
PR 13-NOV-2000; 2000US-0247013P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX
DR WPI; 2001-536777/59.
DR P-PSDB; AAG67391.
XX
PT Nucleic acids capable of encoding human polypeptides having a kinase or
PT kinase-like activity, useful for diagnosing a disease selected from
PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT Alzheimer's disease).
XX
PS Example 1; Fig 1A; 201pp; English.
XX
CC The present sequence encodes a partial human protein kinase. The gene is
CC located at chromosomal position 3p24.2-p21.3. The kinase polypeptides are
CC useful for diagnosing a disease or disorder selected from cancers (e.g.
CC cancers of tissues and cancers of hematopoietic origin), immune-related
CC diseases and disorders, cardiovascular disease, brain or neuronal-
CC associated diseases (e.g. Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis), metabolic disorders, peripheral nervous system
CC diseases, amyotrophic lateral sclerosis, viral infections, infections
CC caused by prions, infections caused by bacteria, infections caused by
CC fungi, ocular diseases, migraines, pain, sexual dysfunction, mood
CC disorders, attention disorders, cognition disorders, hypotension,
CC hypertension, psychotic disorders, dyskinesias, and organ transplant
CC rejection. Kinase inhibitors are useful for treating diseases and
CC disorders described above
XX
SQ Sequence 2562 BP; 792 A; 521 C; 582 G; 667 T; 0 U; 0 Other;

Query Match 63.1%; Score 2299.2; DB 5; Length 2562;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2363; Conservative 0; Mismatches 38; Indels 21; Gaps 2;

```
Qy          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60

Qy         61 ATCTTGTTCCTTGCTTCCTTGGGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 ATCTTGTTCCTTGCTTCCTTGTGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120

Qy        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180

Qy        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240

Qy        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300

Qy        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360

Qy        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420

Qy        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480

Qy        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540

Qy        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600

Qy        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660

Qy        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAAATACAAGAAAATACTTTCTCACTTCAAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAAATACAAGAAAATACTTTCTCACTTCAAGCA 720

Qy        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780

Qy        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840

Qy        841 GCAAAAAGTAATCTATTACAG--------GTAATAAACATGTCTCTTGTCCTTCAGTAT- 891
              |||||||||||||||||||        |   | | |    ||   |||||||||
Db        841 GCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCCTTGAGATTTCTCTTCAGTATG 900

Qy        892 ------------CAAGTTATTGAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATT 939
                          | | |  || |||   |     |   ||||||||||||||||||||
Db        901 GAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACAGACTTGTTTGAGATCTTCATT 960

Qy        940 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 1020

Qy       1000 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1080

Qy       1060 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1140

Qy       1120 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1200

Qy       1180 GTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTCAATTTACATAACCCAGCATTTGGGAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1260

Qy       1240 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1320
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Qy       1300 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1380

Qy       1360 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1440

Qy       1420 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1500

Qy       1480 AGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTA 1539
             ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGGATTGTCCATAGAGATCAGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTA 1560

Qy       1540 ACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTG 1599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACCTCTGTG 1620

Qy       1600 GTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAG 1659
             ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db       1621 GTTGGAACAATCCTGTATTCTTGTCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAG 1680

Qy       1660 GCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTC 1719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTC 1740

Qy       1720 TACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTC 1779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTC 1800

Qy       1780 CCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGAT 1839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGAT 1860

Qy       1840 GCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAA 1899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAA 1920

Qy       1900 TATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGA 1959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGA 1980

Qy       1960 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2040

Qy       2020 CTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGA 2079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGA 2100

Qy       2080 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2160

Qy       2140 GCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTC 2199
             ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       2161 GCCTCCTATGGTAAAGACGAAGACAGGGCCTGTAACGAAATCCTGTCAGATGATAACTTC 2220

Qy       2200 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2280

Qy       2260 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2340

Qy       2320 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2400

Qy       2380 ACAGGATCAAGACCAAGACCAG 2401
```

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             ||||||||||||||||||||||
Db       2401 ACAGGATCAAGACCAAGACCAG 2422
```

RESULT 6
ADN36597
ID ADN36597 standard; DNA; 2562 BP.
XX
AC ADN36597;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human protein kinase-like protein SGK237 coding sequence.
XX
KW ds; gene; cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischemia; reperfusion.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2562
FT /*tag= a
FT /product= "human protein kinase-like protein SGK237"
XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
DR P-PSDB; ADN36596.
XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Example 2; SEQ ID NO 5; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,
CC preventing and treating kinase-related diseases, in particular, diseases
CC associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC autoimmune disorders, retinal detachment, stroke, epilepsy or
CC ischemia/reperfusion. This sequence corresponds to the coding sequence
CC for the protein kinase-like protein SGK237 protein and used in comparison
CC with the HPK3P23 protein kinase of the invention.
XX
SQ Sequence 2562 BP; 792 A; 521 C; 582 G; 667 T; 0 U; 0 Other;

Query Match 63.1%; Score 2299.2; DB 12; Length 2562;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2363; Conservative 0; Mismatches 38; Indels 21; Gaps 2;

```
Qy          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60
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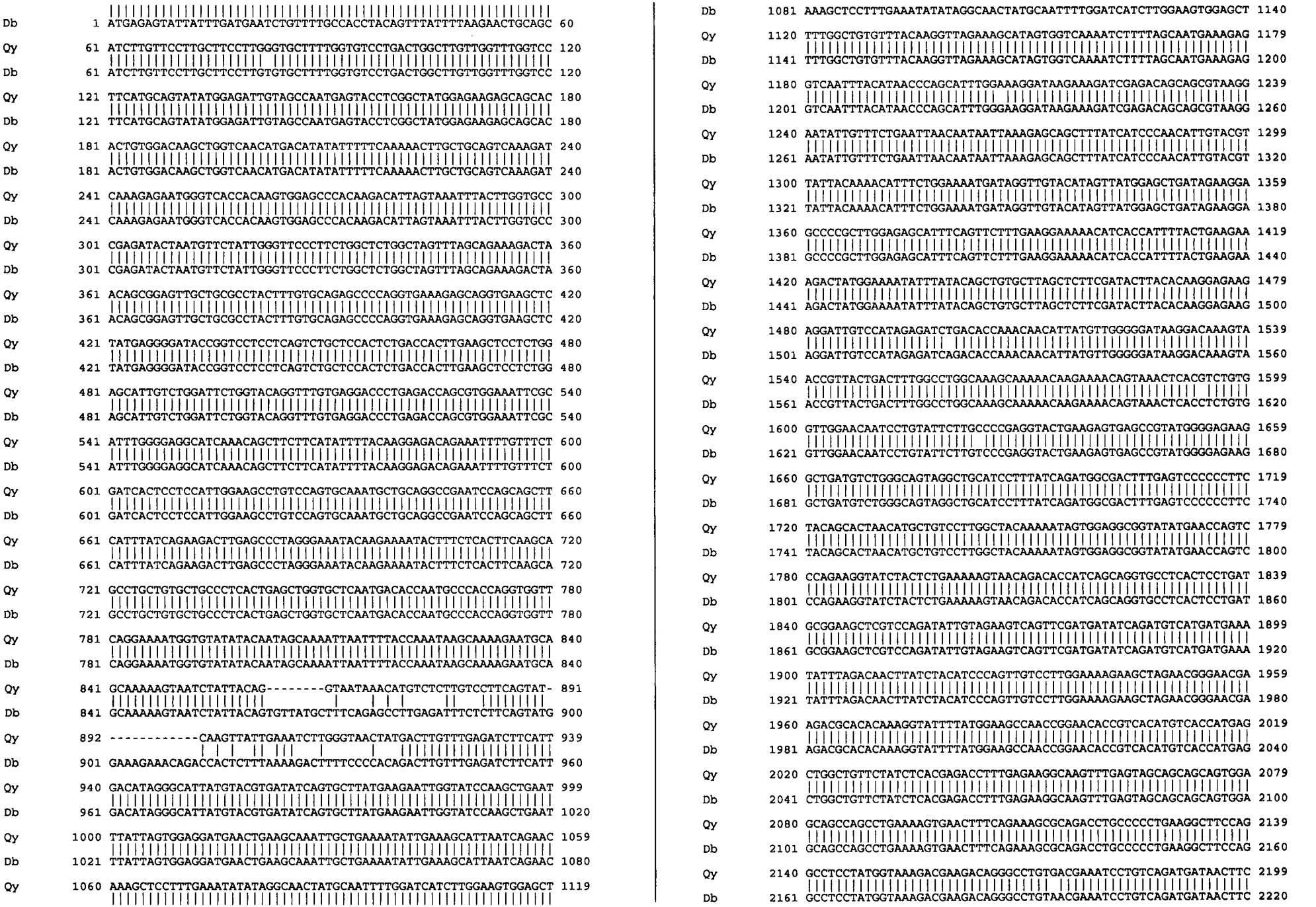

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Qy       2200 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2280

Qy       2260 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2340

Qy       2320 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2400

Qy       2380 ACAGGATCAAGACCAAGACCAG 2401
             |||||||||||||||||||||||
Db       2401 ACAGGATCAAGACCAAGACCAG 2422
```

RESULT 7
ADN36598
ID ADN36598 standard; cDNA; 2043 BP.
XX
AC ADN36598;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human putative Ser/Thr protein kinase D1044.3 cDNA.
XX
KW ds; cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischemia; reperfusion.
XX
OS Homo sapiens.
XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Example 2; SEQ ID NO 6; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,
CC preventing and treating kinase-related diseases, in particular, diseases
CC associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC autoimmune disorders, retinal detachment, stroke, epilepsy or
CC ischemia/reperfusion. This sequence corresponds to the cDNA sequence for
CC a putative Ser/Thr protein kinase D1044.3 and used in comparison with the
CC HPK3P23 protein kinase of the invention.

XX
SQ Sequence 2043 BP; 622 A; 459 C; 462 G; 500 T; 0 U; 0 Other;

Query Match 46.9%; Score 1708.2; DB 12; Length 2043;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 375

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 435

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 495

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 555

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 675

Qy       2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 735

Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 795

Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 855

Qy       2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915

Qy       2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 975

Qy       2343 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 2402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 1035

Qy       2403 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 2462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 1095

Qy       2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 1155

Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 1215

Qy       2583 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 2642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1216 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 1275

Qy       2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 1335

Qy       2703 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 2762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 1395

Qy       2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 1455

Qy       2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 1515

Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 1575

Qy       2943 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 3002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1635

Qy       3003 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 3062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 1695

Qy       3063 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 3122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 1755

Qy       3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 1815

Qy       3183 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 3242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 1875

Qy       3243 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 3302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 1935

Qy       3303 AATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
             ||||||||||||||||||||||||||| | | |
Db       1936 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1968


RESULT 8
ADA53800
ID   ADA53800 standard; cDNA; 2043 BP.
XX
AC   ADA53800;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human coding sequence, SEQ ID 1368.
XX
KW   Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW   Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW   inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX
OS   Homo sapiens.
XX
PN   EP1293569-A2.
XX
PD   19-MAR-2003.
XX
PF   21-MAR-2002; 2002EP-00006586.
XX
PR   14-SEP-2001; 2001JP-00328381.
PR   24-JAN-2002; 2002US-0350435P.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-395539/38.
DR   P-PSDB; ADA55439.
XX
PT   New polynucleotides encoding full-length polypeptides, e.g. secretory
PT   and/or membrane proteins, useful for developing medicines for diseases in
PT   which the gene is involved, or as target molecules for gene therapy.
XX
PS   Claim 1; SEQ ID NO 1368; 205pp; English.
XX
CC   The present invention relates to novel human secretory or membrane
CC   proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC   ADA54071). The coding sequences are useful in the gene therapy of
CC   diseases caused by abnormalities of the proteins, e.g. cancer,
CC   inflammatory diseases, osteoporosis or neurological disease.
XX
SQ   Sequence 2043 BP; 622 A; 458 C; 463 G; 500 T; 0 U; 0 Other;

  Query Match             46.8%;  Score 1705;  DB 10;  Length 2043;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1708;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 375

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        376 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAA 435

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 495

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 555

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 675

Qy       2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 735

Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 795

Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 855

Qy       2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915

Qy       2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 975

Qy       2343 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 2402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 1035

Qy       2403 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 2462
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1036 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCATATGCTCAGGGCCCACATTAA 1095

Qy       2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 1155

Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 1215

Qy       2583 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 2642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 1275

Qy       2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 1335

Qy       2703 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 2762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 1395

Qy       2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 1455

Qy       2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 1515

Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 1575

Qy       2943 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 3002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1635

Qy       3003 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 3062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 1695

Qy       3063 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 3122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 1755

Qy       3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 1815

Qy       3183 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 3242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 1875

Qy       3243 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 3302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 1935

Qy       3303 AATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
             ||||||||||||||||||||||||||| | | |
Db       1936 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1968
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RESULT 9
ADN36599
ID ADN36599 standard; cDNA; 2043 BP.
XX
AC ADN36599;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human cDNA FLJ32685.
XX
KW ds; cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischemia; reperfusion.
XX
OS Homo sapiens.
XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Example 2; SEQ ID NO 7; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,
CC preventing and treating kinase-related diseases, in particular, diseases
CC associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC autoimmune disorders, retinal detachment, stroke, epilepsy or
CC ischemia/reperfusion. This sequence corresponds to the cDNA FLJ32685
CC sequence and used in comparison with the HPK3P23 protein kinase of the
CC invention.
XX
SQ Sequence 2043 BP; 622 A; 458 C; 463 G; 500 T; 0 U; 0 Other;

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  Query Match             46.8%;  Score 1705;  DB 12;  Length 2043;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1708;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 375

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
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Db       376 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAA 435
Qy      1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
Db       436 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 495
Qy      1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
Db       496 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 555
Qy      1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
Db       556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615
Qy      1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
Db       616 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 675
Qy      2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
Db       676 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 735
Qy      2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
Db       736 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 795
Qy      2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
Db       796 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 855
Qy      2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
Db       856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915
Qy      2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
Db       916 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 975
Qy      2343 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 2402
Db       976 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 1035
Qy      2403 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 2462
Db      1036 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCATATGCTCAGGGCCCACATTAA 1095
Qy      2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
Db      1096 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 1155
Qy      2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
Db      1156 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 1215
Qy      2583 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 2642
Db      1216 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 1275
Qy      2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
Db      1276 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 1335
Qy      2703 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 2762
Db      1336 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 1395
Qy      2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
Db      1396 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 1455
Qy      2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
Db      1456 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 1515
Qy      2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
Db      1516 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 1575
Qy      2943 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 3002
Db      1576 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1635
Qy      3003 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 3062
Db      1636 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 1695
Qy      3063 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 3122
Db      1696 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 1755
Qy      3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
Db      1756 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 1815
Qy      3183 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 3242
Db      1816 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 1875
Qy      3243 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 3302
Db      1876 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 1935
Qy      3303 AATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
Db      1936 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1968
```

RESULT 10
ADQ64826
ID ADQ64826 standard; cDNA; 2638 BP.
XX
AC ADQ64826;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human cDNA sequence #1987.
XX
KW ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
DR P-PSDB; ADQ67014.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 1987; 2449pp; English.

```
XX
CC   The invention relates to 2495 novel polynucleotides (I) and their encoded
CC   polypeptides, sequences hybridizing to these nucleotides, sequences
CC   encoding partial polypeptides and sequences having 70% or 90% identity to
CC   the nucleotide and protein sequences. The nucleotides and polypeptides
CC   are useful as diagnostic markers or therapeutic target for the diseases
CC   or morbid states. They are also useful for treating osteoporosis,
CC   neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC   dementia and various cancers. This sequence corresponds to a nucleotide
CC   sequence of the invention.
XX
SQ   Sequence 2638 BP; 819 A; 528 C; 604 G; 687 T; 0 U; 0 Other;

  Query Match             35.8%;  Score 1305.2;  DB 12;  Length 2638;
  Best Local Similarity   91.2%;  Pred. No. 0;
  Matches 1463;  Conservative    0;  Mismatches   33;  Indels  108;  Gaps    3;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 820

Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 880

Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 940

Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
              |||||||||||||||||||||||||||||||||||||||||||||
Db        941 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 1000

Qy        353 ------------------------------------------------------------ 352

Db       1001 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 1060

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 1120

Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 1180

Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 1240

Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 1300

Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 1360

Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 1420

Qy        700 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 1480

Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1481 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 1540

Qy        820 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAG--------GTAATAAACA 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1541 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCC 1600

Qy        872 TGTCTCTTGTCCTTCAGTAT-------------CAAGTTATTGAAATCTTGGGTAACTAT 918
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1601 TTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACA 1660

Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 1720

Qy        979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1721 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1780

Qy       1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1781 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1840

Qy       1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1841 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1900

Qy       1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1901 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGGAAGGATAAGAAA 1960

Qy       1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1961 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 2020

Qy       1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2021 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 2080

Qy       1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2081 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 2140

Qy       1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2141 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 2200

Qy       1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2201 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 2260

Qy       1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2261 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 2320

Qy       1579 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTG 1622
              |||||||||||||||||||||||||||||||||||||||||||
Db       2321 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTG 2364


RESULT 11
ADN36600
ID   ADN36600 standard; cDNA; 1601 BP.
XX
AC   ADN36600;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human cDNA FLJ25966.
XX
KW   ds; cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW   antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW   immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW   anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW   cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW   rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW   cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW   epilepsy; ischemia; reperfusion.
XX
OS   Homo sapiens.
```

XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Example 2; SEQ ID NO 8; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,
CC preventing and treating kinase-related diseases, in particular, diseases
CC associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC autoimmune disorders, retinal detachment, stroke, epilepsy or
CC ischemia/reperfusion. This sequence corresponds to the cDNA FLJ25966
CC sequence and used in comparison with the HPK3P23 protein kinase of the
CC invention.
XX
SQ Sequence 1601 BP; 496 A; 324 C; 373 G; 408 T; 0 U; 0 Other;

Query Match 34.8%; Score 1266.8; DB 12; Length 1601;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1268; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1274 AGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGT 1333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGT 197

Qy       1334 ACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGG 1393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 ACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGG 257

Qy       1394 AAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAG 1453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 AAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAG 317

Qy       1454 CTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACA 1513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACA 377

Qy       1514 TTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAAC 1573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAAC 437

Qy       1574 AAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTAC 1633
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        438 AAGAAAACAGTAAACTCACCTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTAC 497

Qy       1634 TGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATC 1693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 TGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATC 557

Qy       1694 AGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAA 1753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 AGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAA 617

Qy       1754 TAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACA 1813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACA 677

Qy       1814 CCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTT 1873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTT 737

Qy       1874 CGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCT 1933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 CGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCT 797

Qy       1934 TGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACC 1993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 TGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACC 857

Qy       1994 GGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGG 2053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 GGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGG 917

Qy       2054 CAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCG 2113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 CAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCG 977

Qy       2114 CAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTG 2173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 CAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTG 1037

Qy       2174 ACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAG 2233
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1038 ACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAG 1097

Qy       2234 AGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGA 2293
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        1098 AGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCCCTGA 1157

Qy       2294 AAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAAT 2353
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1158 AAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAAT 1217

Qy       2354 CCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTC 2413
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1218 CCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTC 1277

Qy       2414 TTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGG 2473
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1278 TTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGG 1337

Qy       2474 CTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCA 2533
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1338 CTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCA 1397

Qy       2534 AAGATCATGG 2543
             ||||||||||
Db        1398 AAGATCATGG 1407
```

RESULT 12
ACN90120
ID ACN90120 standard; DNA; 1590 BP.
XX
AC ACN90120;
XX
DT 02-DEC-2004 (first entry)
XX
DE Breast cancer related marker, seq id 11270.
XX
KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS Homo sapiens.
XX
PN US2003099974-A1.

XX
PD 29-MAY-2003.
XX
PF 18-JUL-2002; 2002US-00198846.
XX
PR 18-JUL-2001; 2001US-0306220P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2003-787014/74.
XX
PT Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX
PS Disclosure; SEQ ID NO 11270; 36pp; English.
XX
CC The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ Sequence 1590 BP; 504 A; 292 C; 309 G; 483 T; 0 U; 2 Other;

Query Match 19.8%; Score 722.6; DB 11; Length 1590;
Best Local Similarity 99.5%; Pred. No. 1.5e-192;
Matches 725; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2607 GCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATAATCTATAT 2666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATAATCTATAT 60

Qy       2667 CACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAGAGATTCAA 2726
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 CACACAGCTTCCTCCAGCTTCGCACCACAATTTGAAAAGAAGGGTTATAGAGAGATTCAA 120

Qy       2727 GAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATTAAAAAGTT 2786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATTAAAAAGTT 180

Qy       2787 ATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTACCATTTATT 2846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTACCATTTATT 240

Qy       2847 ACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTACCAACCAG 2906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTACCAACCAG 300

Qy       2907 CATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAAGAAGTCCT 2966
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAAGAAGTCCT 360

Qy       2967 TGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCATGGGGGAC 3026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCATGGGGGAC 420

Qy       3027 CAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAG 3086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAG 480

Qy       3087 TGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCT 3146
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCT 540

Qy       3147 AGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCT 3206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCT 600

Qy       3207 GTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATA 3266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATA 660

Qy       3267 CAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCATCTTTTGG 3326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCATCTTTTGG 720

Qy       3327 AGGATTGAG 3335
             ||| | | |
Db         721 AGGGTGGGG 729
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RESULT 13
AAS27199/c
ID AAS27199 standard; cDNA; 861 BP.
XX
AC AAS27199;
XX
DT 07-NOV-2001 (first entry)
XX
DE cDNA encoding novel signal transduction pathway protein, Seq ID 234.
XX
KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS; ss;
KW acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200154733-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001312.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
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PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR P-PSDB; AAU17282.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 234; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
CC AAS27850 represent novel signal transduction pathway protein coding
CC sequences and PCR primers of the invention

```
XX

  Query Match             18.8%;  Score 684.2;  DB 4;  Length 861;
  Best Local Similarity   98.6%;  Pred. No. 7.3e-182;
  Matches  689;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        934 TTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 TTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAG 802

Qy        994 CTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAAT 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 CTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAAT 742

Qy       1054 CAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGT 1113
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        741 CAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGT 682

Qy       1114 GGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATG 622

Qy       1174 AAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 AAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGC 562

Qy       1234 GTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATT 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        561 GTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCMACATT 502

Qy       1294 GTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATA 1353
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        501 GTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATAGTTATGGAGCTGATA 442

Qy       1354 GAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACT 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACT 382

Qy       1414 GAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAG 322

Qy       1474 GAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGAC 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGAC 262

Qy       1534 AAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG 1593
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG 202

Qy       1594 TCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTA 1632
              |||||||||||||||||||||||||||||   | | | |
Db        201 TCTGTGGTTGGAACAATCCTGTATTCTTGATGCAAAGAA 163


RESULT 14
ADB93377/c
ID   ADB93377 standard; cDNA; 861 BP.
XX
AC   ADB93377;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human cDNA encoding a novel protein #224.
XX
KW   ss; gene; human; autoimmune disease; Parkinson's disease; silicosis;
KW   gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW   immunosuppressive agent; adjuvant; enhance immune response;
KW   higher affinity antibody induction;
KW   increased serum immunoglobulin concentration.
XX
OS   Homo sapiens.
XX
PN   US2002168711-A1.
XX
PD   14-NOV-2002.
XX
PF   17-JAN-2001; 2001US-00764868.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   28-JUN-2000; 2000US-0214886P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   22-AUG-2000; 2000US-0226868P.
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PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
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PR   08-DEC-2000; 2000US-0251869P.
XX
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
XX
PI   Rosen CA,  Ruben SM,  Barash SC;
XX
DR   WPI; 2003-719985/68.
DR   P-PSDB; ADB93990.
XX
PT   New isolated polypeptide useful for diagnosing and treating
PT   immunosuppressive conditions such as autoimmune disease and Parkinson's
PT   disease.
XX
PS   Claim 3; SEQ ID NO 234; 345pp; English.
XX
CC   The invention relates to an isolated polypeptide. The polypeptide is
```

CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in The nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents cDNA encoding a novel human protein. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format direct from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020168711.
XX
SQ Sequence 861 BP; 252 A; 176 C; 135 G; 297 T; 0 U; 1 Other;

Query Match 18.8%; Score 684.2; DB 10; Length 861;
Best Local Similarity 98.6%; Pred. No. 7.3e-182;
Matches 689; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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Qy        934 TTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 TTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAG 802

Qy        994 CTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAAT 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 CTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAAT 742

Qy       1054 CAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGT 1113
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        741 CAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGT 682

Qy       1114 GGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATG 622

Qy       1174 AAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 AAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGC 562

Qy       1234 GTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATT 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        561 GTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCMACATT 502

Qy       1294 GTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATA 1353
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        501 GTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATAGTTATGGAGCTGATA 442

Qy       1354 GAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACT 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACT 382

Qy       1414 GAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAG 322

Qy       1474 GAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGAC 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGAC 262
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Qy       1534 AAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG 1593
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG 202

Qy       1594 TCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTA 1632
              |||||||||||||||||||||||||||||  | | | |
Db        201 TCTGTGGTTGGAACAATCCTGTATTCTTGATGCAAAGAA 163
```

RESULT 15
ABK43499
ID ABK43499 standard; cDNA; 861 BP.
XX
AC ABK43499;
XX
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding novel central nervous system protein #79.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001332.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-581633/65.
DR P-PSDB; AAU87169.
XX
PT New isolated nucleic acid encoding a protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as food additives or
PT preservatives.
XX
PS Claim 1; SEQ ID NO 89; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (III) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amylotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

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SUMMARIES

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5	2377.4	65.2	3348	15	US-10-335-711-3	Sequence 3, Appli
6	2299.2	63.1	2562	17	US-10-220-955-2	Sequence 2, Appli
7	2299.2	63.1	2562	17	US-10-684-190-5	Sequence 5, Appli
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ALIGNMENTS

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; Publication No. US20040096889A1
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; APPLICANT: Wyeth
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; TITLE OF INVENTION: KINASE
; FILE REFERENCE: AM101073
; CURRENT APPLICATION NUMBER: US/10/684,190
; CURRENT FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 86
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; ORGANISM: Homo sapiens
US-10-684-190-1

Query Match 100.0%; Score 3644; DB 17; Length 3644;
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Qy      1081 GGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTT 1140
Db      1081 GGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTT 1140

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Db      1141 AGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCA 1200

Qy      1201 TTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACA 1260
Db      1201 TTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACA 1260

Qy      1261 ATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAA 1320
Db      1261 ATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAA 1320

Qy      1321 AATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTC 1380
Db      1321 AATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTC 1380

Qy      1381 AGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATA 1440
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Qy      1441 CAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTG 1500
Db      1441 CAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTG 1500

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Db      1561 GCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCT 1620

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Qy      1801 AAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATT 1860
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Qy      2221 GATACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGT 2280
Db      2221 GATACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGT 2280

Qy      2281 TCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGA 2340
Db      2281 TCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGA 2340

Qy      2341 GGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCA 2400
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Qy       2401 GCTTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATT 2460
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Db       2401 GCTTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATT 2460

Qy       2461 AAGGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATT 2520
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Db       2461 AAGGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATT 2520

Qy       2521 CTTCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCA 2580
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Qy       3181 CTGCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGG 3240
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Qy       3361 TTCGCTACGATGCGGCATCAACAAGGCGGGTGGGAGTTCGCATCACACCAGATCAAGGTG 3420
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RESULT 2
US-10-618-941-27
; Sequence 27, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 3912
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-27

Query Match 74.6%; Score 2719.8; DB 18; Length 3912;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 3031; Conservative 0; Mismatches 37; Indels 249; Gaps 4;

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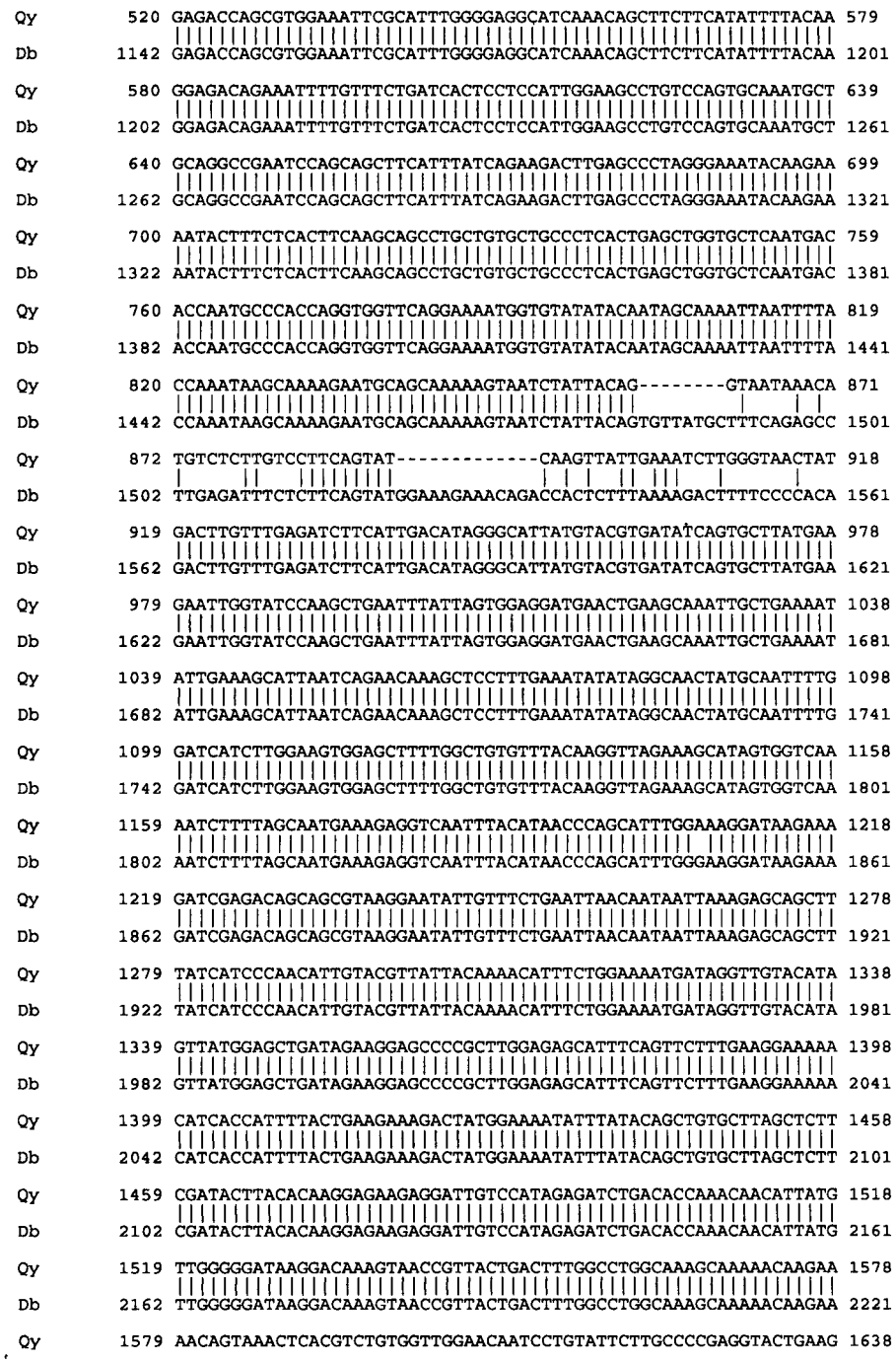
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Db       3521 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3580

Qy       3079 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3581 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3640

Qy       3139 GTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTG 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3641 GTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTG 3700

Qy       3199 GGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACAC 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3701 GGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACAC 3760

Qy       3259 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3761 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3820

Qy       3319 TCTTTTGGAGGATTGAG 3335
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Db       3821 TCTTTTGGAGGGTGGGG 3837


RESULT 3
US-10-335-711-1
; Sequence 1, Application US/10335711
; Publication No. US20030134317A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel E.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 14815, A Human Kinase Family Member and
;  TITLE OF INVENTION:  Uses Therefor
;  FILE REFERENCE: MPI02-002P1RNM
;  CURRENT APPLICATION NUMBER: US/10/335,711
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: 60/345,853
;  PRIOR FILING DATE: 2002-01-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3919
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (183)...(3530)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 3899
;   OTHER INFORMATION: n=a, t, c, or g
US-10-335-711-1

  Query Match           72.9%;  Score 2656.6;  DB 15;  Length 3919;
  Best Local Similarity  90.4%;  Pred. No. 0;
  Matches 2999;  Conservative    0;  Mismatches   39;  Indels  279;  Gaps    4;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 728

Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 788

Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 848

Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        849 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 908

Qy        353 ------------------------------------------------------------ 352

Db        909 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 968

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 1028

Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 1088

Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 1148

Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 1208

Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 1268

Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 1328

Qy        700 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 1388

Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 1448

Qy        820 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGG--------TAATAAACA 871
              ||||||||||||||||||||||||||||||||||||||||||||        |    | |
Db       1449 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCC 1508

Qy        872 TGTCTCTTGTCCTTCAGTAT------------CAAGTTATTGAAATCTTGGGTAACTAT 918
              |    ||   |||||||||            | | |  || |||   |     |
Db       1509 TTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACA 1568

Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 1628

Qy        979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
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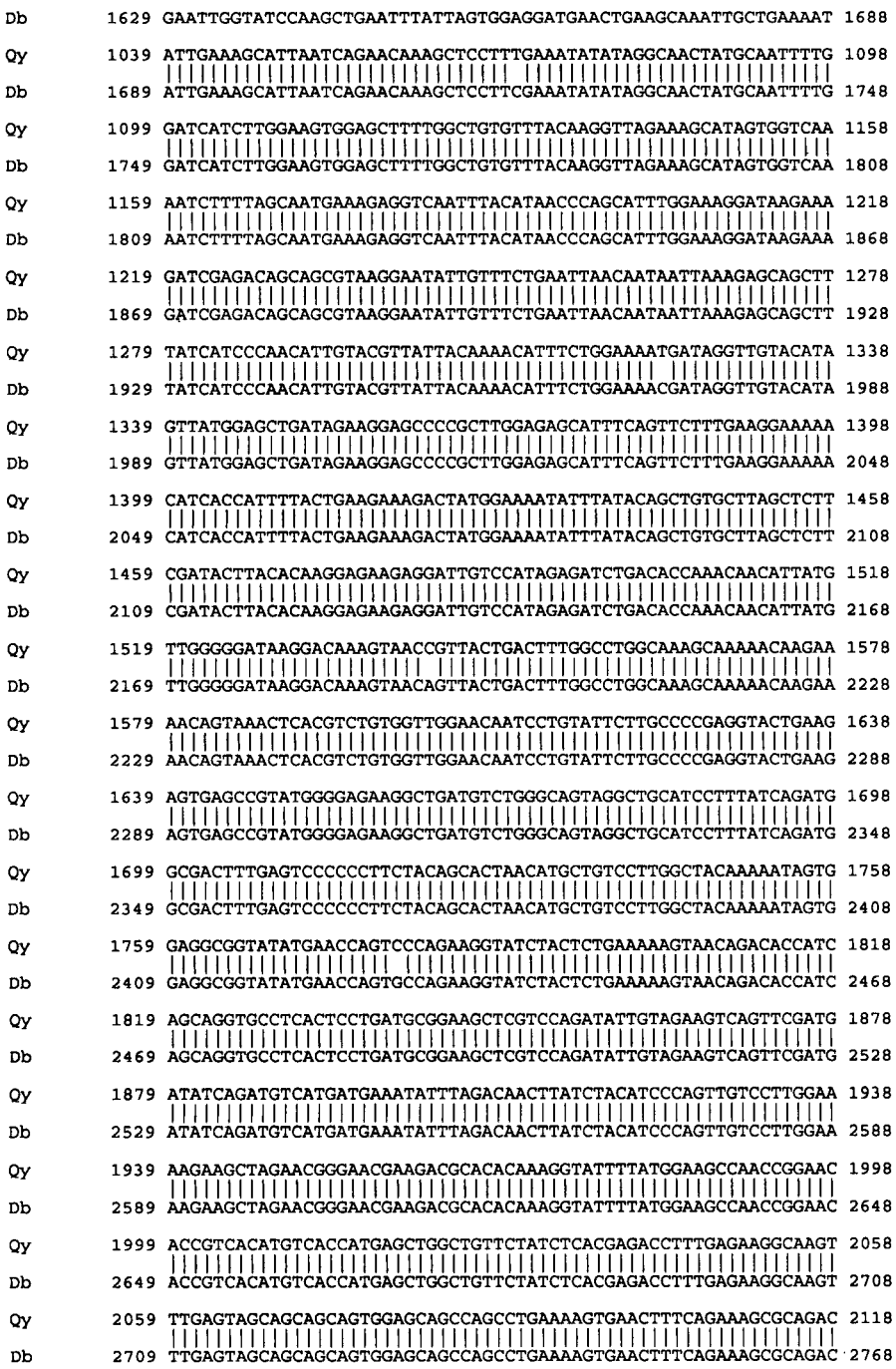
Db 1629 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1688
Qy 1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
Db 1689 ATTGAAAGCATTAATCAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTG 1748
Qy 1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
Db 1749 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1808
Qy 1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
Db 1809 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1868
Qy 1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
Db 1869 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1928
Qy 1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
Db 1929 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATA 1988
Qy 1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
Db 1989 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 2048
Qy 1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
Db 2049 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 2108
Qy 1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
Db 2109 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 2168
Qy 1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
Db 2169 TTGGGGGATAAGGACAAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 2228
Qy 1579 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 1638
Db 2229 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 2288
Qy 1639 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 1698
Db 2289 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 2348
Qy 1699 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 1758
Db 2349 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 2408
Qy 1759 GAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 1818
Db 2409 GAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 2468
Qy 1819 AGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATG 1878
Db 2469 AGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATG 2528
Qy 1879 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 1938
Db 2529 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 2588
Qy 1939 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 1998
Db 2589 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 2648
Qy 1999 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2058
Db 2649 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2708
Qy 2059 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2118
Db 2709 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2768
Qy 2119 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2178
Db 2769 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2828
Qy 2179 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2238
Db 2829 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2888
Qy 2239 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2298
Db 2889 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2948
Qy 2299 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 2358
Db 2949 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 3008
Qy 2359 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTCTTGAC 2418
Db 3009 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACC---------- 3049
Qy 2419 CTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGGCTGAG 2478
Db 3050 ---------- 3049
Qy 2479 TTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCAAAGAT 2538
Db 3050 ---------- 3049
Qy 2539 CATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGGAATTGCTGTGTCCCAG 2598
Db 3050 ----------AGCATCAGCAGGAATTGCTGTGTCCCAG 3077
Qy 2599 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2658
Db 3078 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 3137
Qy 2659 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 2718
Db 3138 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 3197
Qy 2719 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 2778
Db 3198 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 3257
Qy 2779 AAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTAC 2838
Db 3258 AAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTAC 3317
Qy 2839 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 2898
Db 3318 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 3377
Qy 2899 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 2958
Db 3378 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 3437
Qy 2959 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3018
Db 3438 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3497
Qy 3019 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3078
Db 3498 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3557
Qy 3079 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3138
Db 3558 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3617
Qy 3139 GTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTG 3198
Db 3618 GTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTG 3677

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Qy       3199 GGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACAC 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3678 GGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACAC 3737

Qy       3259 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3318
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Db       3738 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3797

Qy       3319 TCTTTTGGAGGATTGAG 3335
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Db       3798 TCTTTTGGAGGGTGGGG 3814
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RESULT 4
US-10-737-450-127
; Sequence 127, Application US/10737450
; Publication No. US20040235071A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Ecsedy, Jeffrey A.
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tighe Nestor, Michelle
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 15986, 2188, 20743, 9148, 9151, 9791, 44252,
; TITLE OF INVENTION: 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411, 15088,
; TITLE OF INVENTION: 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694,
; TITLE OF INVENTION: 15701, 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201,
; TITLE OF INVENTION: 6985, 9883, 12238, 18057, 21617, 39228, 49928, 54476, 62113,
; TITLE OF INVENTION: 64316, 12264, 32362, 58198, 2887, 3205, 8557, 9600, 9693,
; TITLE OF INVENTION: 44867, 53058, 55556, 57658, 2208, 10252, 10302, 14218,
; TITLE OF INVENTION: 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827, 21708,
; TITLE OF INVENTION: 3801, 64698, 2179 OR 13249
; FILE REFERENCE: MPI02-207P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/737,450
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/435,108
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/436,443
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/438,498
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/444,370
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/446,031
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/453,635
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/457,199
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/462,458
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/466,732
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/469,184
; PRIOR FILING DATE: 2003-05-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 3919
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)...(3530)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3919)
; OTHER INFORMATION: n = A,T,C or G
US-10-737-450-127

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  Query Match           72.9%;  Score 2656.6;  DB 18;  Length 3919;
  Best Local Similarity  90.4%;  Pred. No. 0;
  Matches 2999;  Conservative    0;  Mismatches   39;  Indels  279;  Gaps    4;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
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Db        669 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 728

Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 788

Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 848

Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG---------------- 352
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 908

Qy        353 ------------------------------------------------------------ 352

Db        909 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 968

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
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Db        969 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 1028

Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
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Db       1089 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 1148

Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 1208

Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 1268

Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 1328

Qy        700 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 1388

Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 1448

Qy        820 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGG--------TAATAAACA 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCC 1508

Qy        872 TGTCTCTTGTCCTTCAGTAT-------------CAAGTTATTGAAATCTTGGGTAACTAT 918
              |    ||   |||||||||              | | |  || |||   |     |
Db       1509 TTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACA 1568

Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 1628

Qy        979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1629 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1688

Qy       1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
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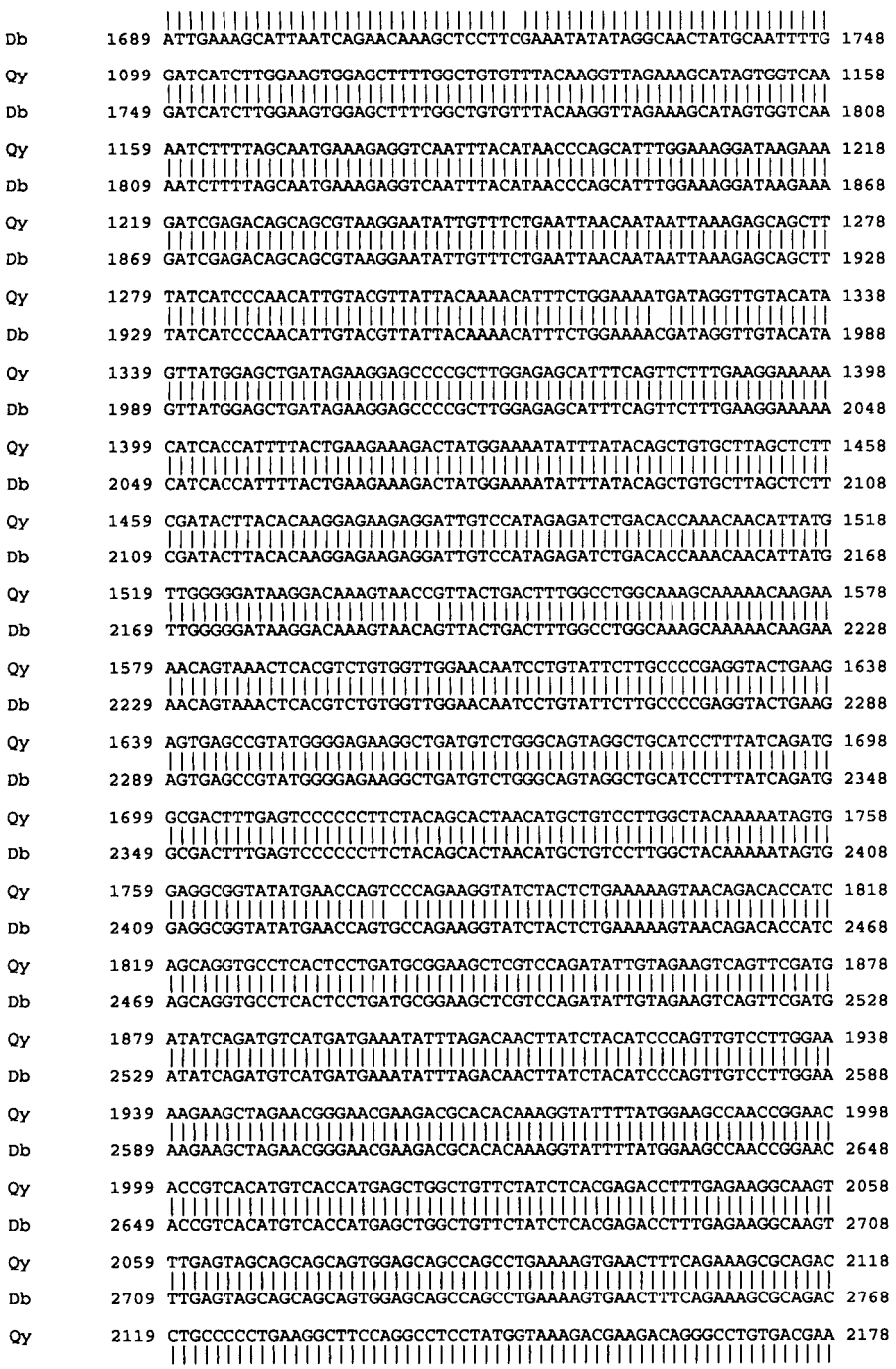
Db 1689 ATTGAAAGCATTAATCAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTG 1748
Qy 1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
Db 1749 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1808
Qy 1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
Db 1809 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1868
Qy 1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
Db 1869 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1928
Qy 1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
Db 1929 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATA 1988
Qy 1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
Db 1989 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 2048
Qy 1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
Db 2049 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 2108
Qy 1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
Db 2109 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 2168
Qy 1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
Db 2169 TTGGGGGATAAGGACAAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 2228
Qy 1579 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 1638
Db 2229 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 2288
Qy 1639 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 1698
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Qy 1699 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 1758
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Qy 1759 GAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 1818
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Qy 1879 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 1938
Db 2529 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 2588
Qy 1939 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 1998
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Qy 1999 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2058
Db 2649 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2708
Qy 2059 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2118
Db 2709 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2768
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Db 2829 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2888
Qy 2239 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2298
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Qy 2299 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 2358
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Db 3009 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACC---------- 3049
Qy 2419 CTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGGCTGAG 2478
Db 3050 ---------- 3049
Qy 2479 TTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCAAAGAT 2538
Db 3050 ---------- 3049
Qy 2539 CATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGGAATTGCTGTGTCCCAG 2598
Db 3050 ----------AGCATCAGCAGGAATTGCTGTGTCCCAG 3077
Qy 2599 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2658
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Qy 2659 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 2718
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Qy 2719 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 2778
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Qy 2899 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 2958
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Db 3438 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3497
Qy 3019 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3078
Db 3498 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3557
Qy 3079 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3138
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RESULT 5
US-10-335-711-3
; Sequence 3, Application US/10335711
; Publication No. US20030134317A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel E.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 14815, A Human Kinase Family Member and
;  TITLE OF INVENTION:  Uses Therefor
;  FILE REFERENCE: MPI02-002P1RNM
;  CURRENT APPLICATION NUMBER: US/10/335,711
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: 60/345,853
;  PRIOR FILING DATE: 2002-01-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3348
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(3348)
US-10-335-711-3

  Query Match             65.2%;  Score 2377.4;  DB 15;  Length 3348;
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  Matches 2718;  Conservative    0;  Mismatches   36;  Indels  279;  Gaps    4;

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Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
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Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
              |||||||||||||||||||||||||||||||||||||||||||||
Db        667 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 726

Qy        353 ------------------------------------------------------------ 352

Db        727 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 786

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
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Db        787 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 846

Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
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Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
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Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
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Db       1147 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 1206

Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
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Qy        872 TGTCTCTTGTCCTTCAGTAT-------------CAAGTTATTGAAATCTTGGGTAACTAT 918
              |    ||   |||||||||              | | |  || |||   |     |
Db       1327 TTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACA 1386

Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
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Db       1387 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 1446

Qy        979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1506

Qy       1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1507 ATTGAAAGCATTAATCAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTG 1566

Qy       1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1626

Qy       1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1627 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1686

Qy       1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1687 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1746

Qy       1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1747 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATA 1806

Qy       1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1807 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1866

Qy       1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1867 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1926

Qy       1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1927 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1986

Qy       1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1987 TTGGGGGATAAGGACAAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 2046

Qy       1579 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 1638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2047 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 2106
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Qy       1639 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 1698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2107 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 2166

Qy       1699 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2167 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 2226

Qy       1759 GAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 1818
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2227 GAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 2286

Qy       1819 AGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1879 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2347 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 2406

Qy       1939 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2407 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 2466

Qy       1999 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2467 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2526

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Db       2527 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2586

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2587 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2646

Qy       2179 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2647 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2706

Qy       2239 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2707 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2766

Qy       2299 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2767 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 2826

Qy       2359 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTCTTGAC 2418
             ||||||||||||||||||||||||||||||||||||||||||
Db       2827 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACC---------------------- 2867

Qy       2419 CTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGGCTGAG 2478

Db       2868 ------------------------------------------------------------ 2867

Qy       2479 TTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCAAAGAT 2538

Db       2868 ------------------------------------------------------------ 2867

Qy       2539 CATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGGAATTGCTGTGTCCCAG 2598
                                                 ||||||||||||||||||||||||||||||
Db       2868 -------------------------------AGCATCAGCAGGAATTGCTGTGTCCCAG 2895

Qy       2599 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2896 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2955

Qy       2659 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 2718
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Db       3136 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 3195

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Db       3196 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 3255

Qy       2959 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3256 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3315

Qy       3019 TGGGGGACCAAGAATCACCCAACCAAAAGATGA 3051
             ||||||||||||||||||||||||||||||||
Db       3316 TGGGGGACCAAGAATCACCCAACCAAAAGATGA 3348
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RESULT 6
US-10-220-955-2
; Sequence 2, Application US/10220955
; Publication No. US20030211989A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602-1401
; CURRENT APPLICATION NUMBER: US/10/220,955
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-955-2

Query Match 63.1%; Score 2299.2; DB 17; Length 2562;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2363; Conservative 0; Mismatches 38; Indels 21; Gaps 2;

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Qy          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60

Qy         61 ATCTTGTTCCTTGCTTCCTTGGGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCTTGTTCCTTGCTTCCTTGTGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120

Qy        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180

Qy        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240

Qy        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300

Qy        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360
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Db        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360
Qy        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420
Db        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420
Qy        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480
Db        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480
Qy        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540
Db        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540
Qy        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600
Db        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600
Qy        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660
Db        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660
Qy        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720
Db        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720
Qy        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780
Db        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780
Qy        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840
Db        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840
Qy        841 GCAAAAAGTAATCTATTACAG--------GTAATAAACATGTCTCTTGTCCTTCAGTAT- 891
Db        841 GCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCCTTGAGATTTCTCTTCAGTATG 900
Qy        892 ------------CAAGTTATTGAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATT 939
Db        901 GAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACAGACTTGTTTGAGATCTTCATT 960
Qy        940 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 999
Db        961 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 1020
Qy       1000 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1059
Db       1021 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1080
Qy       1060 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1119
Db       1081 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1140
Qy       1120 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1179
Db       1141 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1200
Qy       1180 GTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1239
Db       1201 GTCAATTTACATAACCCAGCATTTGGGAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1260
Qy       1240 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1299
Db       1261 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1320
Qy       1300 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1359
Db       1321 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1380
Qy       1360 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1419
Db       1381 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1440
Qy       1420 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1479
Db       1441 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1500
Qy       1480 AGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTA 1539
Db       1501 AGGATTGTCCATAGAGATCAGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTA 1560
Qy       1540 ACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTG 1599
Db       1561 ACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACCTCTGTG 1620
Qy       1600 GTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAG 1659
Db       1621 GTTGGAACAATCCTGTATTCTTGTCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAG 1680
Qy       1660 GCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTC 1719
Db       1681 GCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTC 1740
Qy       1720 TACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTC 1779
Db       1741 TACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTC 1800
Qy       1780 CCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGAT 1839
Db       1801 CCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGAT 1860
Qy       1840 GCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAA 1899
Db       1861 GCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAA 1920
Qy       1900 TATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGA 1959
Db       1921 TATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGA 1980
Qy       1960 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2019
Db       1981 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2040
Qy       2020 CTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGA 2079
Db       2041 CTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGA 2100
Qy       2080 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2139
Db       2101 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2160
Qy       2140 GCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTC 2199
Db       2161 GCCTCCTATGGTAAAGACGAAGACAGGGCCTGTAACGAAATCCTGTCAGATGATAACTTC 2220
Qy       2200 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2259
Db       2221 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2280
Qy       2260 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2319
Db       2281 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2340
Qy       2320 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2379
Db       2341 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2400
Qy       2380 ACAGGATCAAGACCAAGACCAG 2401
Db       2401 ACAGGATCAAGACCAAGACCAG 2422
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RESULT 7
US-10-684-190-5

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; Sequence 5, Application US/10684190
; Publication No. US20040096889A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
;  TITLE OF INVENTION:  KINASE
;  FILE REFERENCE: AM101073
;  CURRENT APPLICATION NUMBER: US/10/684,190
;  CURRENT FILING DATE:  2003-10-10
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 2562
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-684-190-5

  Query Match             63.1%;  Score 2299.2;  DB 17;  Length 2562;
  Best Local Similarity   97.6%;  Pred. No. 0;
  Matches 2363;  Conservative    0;  Mismatches   38;  Indels   21;  Gaps    2;

Qy          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60

Qy         61 ATCTTGTTCCTTGCTTCCTTGGGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 ATCTTGTTCCTTGCTTCCTTGTGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120

Qy        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180

Qy        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240

Qy        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300

Qy        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360

Qy        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420

Qy        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480

Qy        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540

Qy        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600

Qy        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660

Qy        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720

Qy        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780

Qy        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840

Qy        841 GCAAAAAGTAATCTATTACAG--------GTAATAAACATGTCTCTTGTCCTTCAGTAT- 891
              |||||||||||||||||||||        |     | | |    ||  ||||||||
Db        841 GCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCCTTGAGATTTCTCTTCAGTATG 900

Qy        892 ------------CAAGTTATTGAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATT 939
                         | | |  || |||  |     |    ||||||||||||||||||||
Db        901 GAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACAGACTTGTTTGAGATCTTCATT 960

Qy        940 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 1020

Qy       1000 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1080

Qy       1060 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1140

Qy       1120 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1200

Qy       1180 GTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1239
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1201 GTCAATTTACATAACCCAGCATTTGGGAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1260

Qy       1240 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1320

Qy       1300 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1380

Qy       1360 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1440

Qy       1420 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1500

Qy       1480 AGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTA 1539
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1501 AGGATTGTCCATAGAGATCAGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTA 1560

Qy       1540 ACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTG 1599
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1561 ACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACCTCTGTG 1620

Qy       1600 GTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAG 1659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1621 GTTGGAACAATCCTGTATTCTTGTCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAG 1680

Qy       1660 GCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTC 1719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTC 1740

Qy       1720 TACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTC 1779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTC 1800

Qy       1780 CCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGAT 1839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGAT 1860

Qy       1840 GCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAA 1899
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Db       1861 GCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATGAAA 1920

Qy       1900 TATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGA 1959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGA 1980

Qy       1960 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2040

Qy       2020 CTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGA 2079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGA 2100

Qy       2080 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2160

Qy       2140 GCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTC 2199
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       2161 GCCTCCTATGGTAAAGACGAAGACAGGGCCTGTAACGAAATCCTGTCAGATGATAACTTC 2220

Qy       2200 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCG 2280

Qy       2260 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAG 2340

Qy       2320 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGA 2400

Qy       2380 ACAGGATCAAGACCAAGACCAG 2401
             |||||||||||||||||||||||
Db       2401 ACAGGATCAAGACCAAGACCAG 2422


RESULT 8
US-10-684-190-6
; Sequence 6, Application US/10684190
; Publication No. US20040096889A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
;  TITLE OF INVENTION:  KINASE
;  FILE REFERENCE: AM101073
;  CURRENT APPLICATION NUMBER: US/10/684,190
;  CURRENT FILING DATE:  2003-10-10
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-684-190-6

  Query Match             46.9%;  Score 1708.2;  DB 17;  Length 2043;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1710;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
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Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 375

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
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Db        376 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 435

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 495

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         496 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 555

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         616 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 675

Qy       2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         676 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 735

Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
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Db         736 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 795

Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
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Db         796 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 855

Qy       2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
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Db         856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915

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Db         976 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 1035

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Db        1036 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 1095

Qy       2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
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Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
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Qy       2703 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 2762
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Qy       2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
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Qy       2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
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Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
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Db       1576 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1635

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Db       1696 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 1755

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Qy       3183 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 3242
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Db       1936 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1968
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RESULT 9
US-10-094-749-1368
; Sequence 1368, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1368
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1368

Query Match 46.8%; Score 1705; DB 17; Length 2043;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
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Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
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             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        376 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAA 435

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 495

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 555

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
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Db        736 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 795

Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
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Qy       2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
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Db        856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915

Qy       2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
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Db        916 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 975

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Db        976 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 1035

Qy       2403 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 2462
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Db       1036 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCATATGCTCAGGGCCCACATTAA 1095

Qy       2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
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Db       1096 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 1155

Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 1215

Qy       2583 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 2642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 1275

Qy       2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
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Db       1276 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 1335

Qy       2703 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 2762
Db       1336 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 1395

Qy       2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
Db       1396 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 1455

Qy       2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
Db       1456 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 1515

Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
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Qy       2943 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 3002
Db       1576 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1635

Qy       3003 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 3062
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Qy       3063 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 3122
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Qy       3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
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Db       1816 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 1875

Qy       3243 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 3302
Db       1876 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 1935

Qy       3303 AATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
Db       1936 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1968


RESULT 10
US-10-684-190-7
; Sequence 7, Application US/10684190
; Publication No. US20040096889A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
;  TITLE OF INVENTION:  KINASE
;  FILE REFERENCE: AM101073
;  CURRENT APPLICATION NUMBER: US/10/684,190
;  CURRENT FILING DATE:  2003-10-10
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-684-190-7

  Query Match             46.8%;  Score 1705;  DB 17;  Length 2043;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1708;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682

Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
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Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
Db        376 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAA 435

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
Db        436 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 495

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
Db        496 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 555

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
Db        556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
Db        616 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 675

Qy       2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
Db        676 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 735

Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
Db        736 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 795

Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
Db        796 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 855

Qy       2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
Db        856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915

Qy       2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
Db        916 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 975

Qy       2343 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 2402
Db        976 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 1035

Qy       2403 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 2462
Db       1036 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCATATGCTCAGGGCCCACATTAA 1095

Qy       2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
Db       1096 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 1155

Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
Db       1156 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 1215

Qy       2583 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 2642
Db       1216 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 1275

Qy       2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
Db       1276 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 1335

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Qy       2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
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Db       1396 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 1455

Qy       2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 1515

Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 1575

Qy       2943 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 3002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1635

Qy       3003 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 3062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 1695

Qy       3063 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 3122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 1755

Qy       3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 1815

Qy       3183 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 3242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 1875

Qy       3243 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 3302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 1935

Qy       3303 AATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
             |||||||||||||||||||||||||| | | |
Db       1936 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1968
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RESULT 11
US-10-425-114-26288
; Sequence 26288, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26288
; LENGTH: 1835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-205-A2_FLI
US-10-425-114-26288

Query Match 37.2%; Score 1356.2; DB 17; Length 1835;
Best Local Similarity 89.8%; Pred. No. 0;
Matches 1539; Conservative 0; Mismatches 3; Indels 171; Gaps 1;

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Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 298

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 358

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 418

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 478

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 538

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 598

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 658

Qy       2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 718

Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 778

Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 838

Qy       2223 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 2282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 898

Qy       2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 958

Qy       2343 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 2402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACC--- 1015

Qy       2403 TTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAA 2462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 ---------------------------------------------------------- 1015

Qy       2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 ---------------------------------------------------------- 1015

Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
             ||||||||||||                                              ||||||||||||
Db       1016 ----------------------------------------------------AGCATCAGCAGG 1027

Qy       2583 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 2642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 AATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAAT 1087

Qy       2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 1147

Qy       2703 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 2762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 AAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAA 1207
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Qy       2763 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 2822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 TTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTT 1267

Qy       2823 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 2882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAA 1327

Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 1387

Qy       2943 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 3002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 GCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAG 1447

Qy       3003 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 3062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 GTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCAT 1507

Qy       3063 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 3122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 TTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAA 1567

Qy       3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 1627

Qy       3183 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 3242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1628 GCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGC 1687

Qy       3243 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 3302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 TTCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAA 1747

Qy       3303 AATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
             ||||||||||||||||||||||||||| | | |
Db       1748 AATGCTGCAAAATTCATCTTTTGGAGGGTGGGG 1780


RESULT 12
US-10-684-190-8
; Sequence 8, Application US/10684190
; Publication No. US20040096889A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
;  TITLE OF INVENTION:  KINASE
;  FILE REFERENCE: AM101073
;  CURRENT APPLICATION NUMBER: US/10/684,190
;  CURRENT FILING DATE:  2003-10-10
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 1601
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-684-190-8

  Query Match             34.8%;  Score 1266.8;  DB 17;  Length 1601;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1268;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1274 AGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGT 1333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGT 197

Qy       1334 ACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGG 1393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         198 ACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGG 257

Qy       1394 AAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAG 1453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 AAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAG 317

Qy       1454 CTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACA 1513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 CTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACA 377

Qy       1514 TTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAAC 1573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         378 TTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAAC 437

Qy       1574 AAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTAC 1633
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         438 AAGAAAACAGTAAACTCACCTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTAC 497

Qy       1634 TGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATC 1693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         498 TGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATC 557

Qy       1694 AGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAA 1753
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         558 AGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAA 617

Qy       1754 TAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACA 1813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         618 TAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACA 677

Qy       1814 CCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTT 1873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         678 CCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTT 737

Qy       1874 CGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCT 1933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         738 CGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCT 797

Qy       1934 TGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACC 1993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         798 TGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACC 857

Qy       1994 GGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGG 2053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         858 GGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGG 917

Qy       2054 CAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCG 2113
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         918 CAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCG 977

Qy       2114 CAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTG 2173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         978 CAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTG 1037

Qy       2174 ACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAG 2233
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1038 ACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAG 1097

Qy       2234 AGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGA 2293
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         1098 AGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCCCTGA 1157

Qy       2294 AAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAAT 2353
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1158 AAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAAT 1217

Qy       2354 CCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTC 2413
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1218 CCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTC 1277

Qy       2414 TTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGG 2473
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1278 TTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGG 1337

Qy       2474 CTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCA 2533
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Db       1338 CTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCA 1397

Qy       2534 AAGATCATGG 2543
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Db       1398 AAGATCATGG 1407


RESULT 13
US-10-198-846-11270
; Sequence 11270, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11270
;   LENGTH: 1590
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1589, 1590
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11270

  Query Match             19.8%;  Score 722.6;  DB 14;  Length 1590;
  Best Local Similarity   99.5%;  Pred. No. 1.1e-188;
  Matches  725;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2607 GCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATAATCTATAT 2666
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATAATCTATAT 60

Qy       2667 CACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAGAGATTCAA 2726
                 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACACAGCTTCCTCCAGCTTCGCACCACAATTTGAAAAGAAGGGTTATAGAGAGATTCAA 120

Qy       2727 GAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATTAAAAAGTT 2786
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATTAAAAAGTT 180

Qy       2787 ATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTACCATTTATT 2846
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTACCATTTATT 240

Qy       2847 ACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTACCAACCAG 2906
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTACCAACCAG 300

Qy       2907 CATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAAGAAGTCCT 2966
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAAGAAGTCCT 360

Qy       2967 TGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCATGGGGGAC 3026
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCATGGGGGAC 420

Qy       3027 CAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAG 3086
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAG 480

Qy       3087 TGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCT 3146
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCT 540

Qy       3147 AGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCT 3206
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCT 600

Qy       3207 GTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATA 3266
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATA 660

Qy       3267 CAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCATCTTTTGG 3326
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCATCTTTTGG 720

Qy       3327 AGGATTGAG 3335
                 ||| | | |
Db        721 AGGGTGGGG 729


RESULT 14
US-09-764-868-234/c
; Sequence 234, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ32
;  CURRENT APPLICATION NUMBER: US/09/764,868
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 1510
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-868-234

  Query Match             18.8%;  Score 684.2;  DB 9;  Length 861;
  Best Local Similarity   98.6%;  Pred. No. 3.1e-178;
  Matches  689;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        934 TTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAG 993
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 TTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAG 802

Qy        994 CTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAAT 1053
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 CTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAAT 742

Qy       1054 CAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGT 1113
                 |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 CAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGT 682

Qy       1114 GGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATG 1173
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATG 622

Qy       1174 AAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGC 1233
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 AAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGC 562

Qy       1234 GTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATT 1293
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        561 GTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCMACATT 502

Qy       1294 GTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATA 1353
                 |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        501 GTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATAGTTATGGAGCTGATA 442

Qy       1354 GAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACT 1413
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACT 382

Qy        1414 GAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 GAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAG 322

Qy        1474 GAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGAC 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 GAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGAC 262

Qy        1534 AAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG 1593
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 AAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG 202

Qy        1594 TCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTA 1632
              |||||||||||||||||||||||||||||    | | | |
Db         201 TCTGTGGTTGGAACAATCCTGTATTCTTGATGCAAAGAA 163


RESULT 15
US-09-764-875-89
; Sequence 89, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ02
;  CURRENT APPLICATION NUMBER: US/09/764,875
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 1249
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-875-89

  Query Match            18.1%;  Score 660;  DB 11;  Length 861;
  Best Local Similarity  98.5%;  Pred. No. 1.6e-171;
  Matches  666;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         957 ACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGA 1016
               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           6 AGGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGA 65

Qy        1017 ACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATA 1076
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          66 ACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAACAAAGCTCCTTCGAAATA 125

Qy        1077 TATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAA 1136
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         126 TATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAA 185

Qy        1137 GGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCC 1196
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         186 GGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCC 245

Qy        1197 AGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATT 1256
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         246 AGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATT 305

Qy        1257 AACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCT 1316
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         306 AACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCT 365

Qy        1317 GGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCA 1376
               |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         366 GGAAAACGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCA 425

Qy        1377 TTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATT 1436
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         426 TTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATT 485

Qy        1437 TATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGA 1496
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         486 TATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGA 545

Qy        1497 TCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGG 1556
               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         546 TCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACAGTTACTGACTTTGG 605

Qy        1557 CCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTA 1616
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         606 CCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTA 665

Qy        1617 TTCTTGCCCCGAGGTA 1632
               ||||||    | | | |
Db         666 TTCTTGATGCAAAGAA 681


Search completed: May 12, 2005, 23:59:56
Job time : 1349 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2005, 18:16:14 ; Search time 7356 Seconds
(without alignments)
18856.199 Million cell updates/sec

Title: PCT-US03-32302-1
Perfect score: 3644
Sequence: 1 atgagagtattatttgatga.....acccatgcggaatccactag 3644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	581.4	16.0	859	6	CD106458	CD106458 AGENCOURT
	2	503.2	13.8	799	5	BU748040	BU748040 CH3#017_D
c	3	499.2	13.7	581	1	AI652681	AI652681 wb30e08.x
	4	473.4	13.0	741	6	BY741024	BY741024 BY741024
c	5	457.4	12.6	664	5	BM976126	BM976126 UI-CF-EN1
c	6	441.2	12.1	523	1	AI962584	AI962584 wq54a01.x
	7	425	11.7	831	5	BU568655	BU568655 AGENCOURT
c	8	418.2	11.5	508	1	AA954906	AA954906 op01b04.s
	9	415	11.4	441	9	AY404298	AY404298 Homo sapi
	10	407.4	11.2	682	4	BG717420	BG717420 602689765
c	11	401	11.0	755	5	BM976173	BM976173 UI-CF-EN1
c	12	385.2	10.6	464	1	AA889152	AA889152 ak25c10.s
c	13	384	10.5	476	1	AA429606	AA429606 zw75f09.s
	14	363.4	10.0	472	7	CR738506	CR738506 CR738506
	15	337.4	9.3	824	5	BX722244	BX722244 BX722244
	16	327	9.0	327	1	AA430250	AA430250 zw65g03.r
c	17	300.4	8.2	495	1	AI149647	AI149647 qf37b05.x
c	18	300.2	8.2	389	1	AA843473	AA843473 aj54d10.s
	19	299.4	8.2	325	5	BU102129	BU102129 PRODG1GID
	20	294	8.1	964	5	BU154882	BU154882 AGENCOURT
c	21	287.2	7.9	369	1	AI611061	AI611061 tt16g10.x
	22	283.4	7.8	441	9	AY404299	AY404299 Pan trogl
	23	226.4	6.2	285	9	AY404300	AY404300 Mus muscu
	24	188.6	5.2	602	9	CE479324	CE479324 tigr-gss-
c	25	164.4	4.5	777	9	CC904276	CC904276 t012o14ba
c	26	154	4.2	360	1	AA430041	AA430041 zw65g03.s
	27	152.2	4.2	646	6	CA371641	CA371641 652175 NC
	28	152.2	4.2	714	6	CA342280	CA342280 672120 NC
c	29	146	4.0	572	8	AQ486417	AQ486417 RPCI-11-2
c	30	143.4	3.9	537	8	AQ693849	AQ693849 HS_5483_A
c	31	143.4	3.9	557	8	AQ718935	AQ718935 HS_5513_B
c	32	141.8	3.9	382	8	B87671	B87671 RPCI11-30A1
c	33	140.2	3.8	393	8	CC061026	CC061026 MUGQ_CH25
c	34	131.2	3.6	485	8	BH900364	BH900364 UP_478-1I
c	35	131.2	3.6	575	8	AQ633949	AQ633949 RPCI-11-4
	36	130	3.6	252	7	CR743590	CR743590 CR743590
	37	126.4	3.5	667	2	AW372558	AW372558 PM2-BT034
	38	113.8	3.1	624	7	CO064746	CO064746 est_k_bre
	39	113	3.1	396	7	T08896	T08896 EST06788 In
c	40	106.4	2.9	651	8	AZ378698	AZ378698 1M0133N01
c	41	100.4	2.8	335	7	CO941351	CO941351 UMC-peov3
	42	97.4	2.7	2873	3	AK004925	AK004925 Mus muscu
	43	95.8	2.6	921	9	AY414602	AY414602 Mus muscu
	44	95.8	2.6	1496	3	AK011519	AK011519 Mus muscu
	45	95.8	2.6	2136	3	AK075717	AK075717 Mus muscu

ALIGNMENTS

RESULT 1
CD106458
LOCUS CD106458 859 bp mRNA linear EST 15-MAY-2003
DEFINITION AGENCOURT_14018718 NIH_MGC_179 Homo sapiens cDNA clone IMAGE:30368322 5', mRNA sequence.
ACCESSION CD106458
VERSION CD106458.1 GI:30759632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM430 row: o column: 19
High quality sequence stop: 668.
FEATURES Location/Qualifiers
source 1. .859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30368322"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed); Site_2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 16.0%; Score 581.4; DB 6; Length 859;
Best Local Similarity 99.8%; Pred. No. 6.5e-150;
Matches 582; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1822 AGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATA 1881
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATA 198

Qy       1882 TCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAG 1941
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAG 258

Qy       1942 AAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACC 2001
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 AAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACC 318

Qy       2002 GTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTG 2061
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGTTTG 378

Qy       2062 AGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTG 2121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 AGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTG 438

Qy       2122 CCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAAATC 2181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAAATC 498

Qy       2182 CTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGAT 2241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTAGAT 558

Qy       2242 GATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCT 2301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAATCT 618

Qy       2302 ACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACA 2361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAAACA 678

Qy       2362 AGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTT 2404
             |||||||||||||||||||||||||||||||||||||||||| |
Db        679 AGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCAT 721
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RESULT 2
BU748040
LOCUS       BU748040                799 bp    mRNA    linear   EST 10-OCT-2002
DEFINITION  CH3#017_D03T7 Canine heart normalized cDNA Library in pBluescript
            Canis familiaris cDNA clone CH3#017_D03 5', mRNA sequence.
ACCESSION   BU748040
VERSION     BU748040.1  GI:23699642
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 799)
  AUTHORS   Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
  TITLE     Expressed sequence tags from Canine heart
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: CH3#017_D03T3
            Contact: George AL
            Division of Genetic Medicine
            Vanderbilt University
            529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
            Tel: 615 936 2660
            Fax: 615 936 2661
            Email: al.george@vanderbilt.edu
            Insert Length: 1821   Std Error: 0.00
            Seq primer: T7: TAATACGACTCACTATAGGG
            High quality sequence start: 91
            High quality sequence stop: 685.
FEATURES             Location/Qualifiers
     source          1. .799
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                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="CH3#017_D03"
                     /tissue_type="heart"
                     /cell_type="heart"
                     /dev_stage="mixed developmental stages (adult, 30 day - 40
                     day fetal)"
                     /clone_lib="Canine heart normalized cDNA Library in
                     pBluescript"
                     /note="Organ: heart; Vector: pBluescript; Site_1: 5' of
                     vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
                     dog heart (adult, 30 day - 40 day fetal), right and left
                     atria and ventricle. Dog breed - mixed (beagle, German
                     shepherd,  pointer, Irish setter). Library construction:
                     oligo-dT primed"
ORIGIN
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  Query Match           13.8%;  Score 503.2;  DB 5;  Length 799;
  Best Local Similarity  85.2%;  Pred. No. 3.9e-128;
  Matches  598;  Conservative    0;  Mismatches   98;  Indels    6;  Gaps    3;

Qy       2572 GCATCAGCAGGAATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAG 2631
             | ||| || || |||||||||||||||||||||||| || ||||||||||||||||||||
Db         83 GGATCTGCGGGGATTGCTGTGTCCCAGAGGAAAGTACGACAGATCAGTGATCCTATTCAG 142

Qy       2632 CAGATATTAATTCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCAC 2691
             ||||| |||||||||||||||||| |||||||||| ||||| ||||||||||||||||||
Db        143 CAGATCTTAATTCAGCTGCACAAAATCATCTATATCACCCAGCTCCCTCCAGCTTTGCAC 202

Qy       2692 CACAATTTGAAAAGAAGGGTTATAGAGAGATTCAAGA-AATCCCTCTTCAGCCAGCAGAG 2750
             |||||||||||||| |||||||||||||||||||| |     ||||||||||||||||
Db        203 CACAATTTGAAAAGAGGGGTTATAGAGAGATTCAAGAGAGGGGGTCTTCAGCCAGCAGAG 262

Qy       2751 TAACCCTTGTAATTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGAT 2810
             |||||||| |||||||||||||||||||||||||||||||||||||| |||||||||||| ||
Db        263 TAACCCTTGCAATTTGAAATCTGAAATTAAAAAGTTATCTGAGGGATCTCCAGAACCAAT 322

Qy       2811 TGAGCCCAACTTTTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAG 2870
             |||||||||||||||||| |||||||||||||||||||| |||||| ||||||||||||
Db        323 CGAGCCCAACTTTTTCACAACAGATTACCATTTATTACATCATTCATCAGGTGGAAACAG 382

Qy       2871 CCTGTCCCCAAATGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAAC 2930
             |||||||||| | || ||  ||||| | |  |||||| |||| |  ||||| |||||||||
Db        383 CCTGTCCCCAGACGAACCAGCAGGTCTGCGTACCAGCTTTGATTCAGAGGAGGGAATAAC 442

Qy       2931 ATATGAACAGATGCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTT 2990
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||
Db        443 ATATGAACAGATGCAGACTGTGATTGAAGAAGTCCTAGAGGAAAGTGGTTATTACAACTT 502

Qy       2991 TACATCTAACAGGTATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATG 3050
             |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Db        503 TACATCTAACAGATATCACTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATG 562

Qy       3051 AAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAG 3110
             ||||  |||||||||||| |||||||  |||||  ||||||||||||||| ||||||||
Db        563 AAAACCCTGCATTTTGAATGGACTTCGTTTTCCTAGTGAAGTTCAAGTTCTAGACTTCAG 622

Qy       3111 CCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCTAG-AGGGTGTGGAAAAGACCAAGA 3169
             |     | | |||||||||||||||||||| |||||| | || ||||||||||| ||||||
Db        623 C----TCTACCAGATGCCCAAGGATTGGGAGCTGCTGGAAGAGTGTGGAAAACACCAAGA 678

Qy       3170 TGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGC 3229
             || |||||  ||  |||| | ||| | ||| |||||||||||  | ||| || | || ||
Db        679 TGTCATGGAACCACCAGGGCCTCTCTGTGGAGGTCCTGTGCTAGGTTATGTGGCCGCGGC 738

Qy       3230 GGTACTTGAGGGCTTCATTGCCAGAACACATTATATACAGGA 3271
              | |  || ||||   |    ||   || |   || | | |
Db        739 AGCATGCGAAGGCTCTGTACGAAGGCTACCTCGGATGCGGTA 780
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```
RESULT 3
AI652681/c
LOCUS       AI652681                581 bp    mRNA    linear   EST 17-DEC-1999
```

```
DEFINITION  wb30e08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307206 3',
            mRNA sequence.
ACCESSION   AI652681
VERSION     AI652681.1  GI:4736660
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 686   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 450.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2307206"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GC6"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match           13.7%;  Score 499.2;  DB 1;  Length 581;
  Best Local Similarity   99.4%;  Pred. No. 4.5e-127;
  Matches  501;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2832 AGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTAC 2891
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 AGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTAC 522

Qy       2892 AGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGT 2951
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 AGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGT 462

Qy       2952 GATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTC 3011
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTC 402

Qy       3012 CTATCCATGGGGGACCAAGAATCACCCAACCAAAAAGATGAAAATGCTGCATTTTGAGTGG 3071
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 CTATCCATGGGGGACCAAGAATCACCCAACCAAAAAGATGAAAATGCTGCATTTTGAGTGG 342

Qy       3072 ACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAA 3131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAA 282

Qy       3132 GGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTT 3191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTT 222

Qy       3192 CTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCC 3251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCC 162

Qy       3252 AGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCA 3311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 AGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCA 102

Qy       3312 AAATTCATCTTTTGGAGGATTGAG 3335
             ||||||||||||||||||| | | |
Db        101 AAATTCATCTTTTGGAGGGTGGGG 78


RESULT 4
BY741024
LOCUS       BY741024                741 bp    mRNA    linear   EST 31-DEC-2002
DEFINITION  BY741024 RIKEN full-length enriched, melanocyte Mus musculus cDNA
            clone G270071A07 5', mRNA sequence.
ACCESSION   BY741024
VERSION     BY741024.1  GI:27165648
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
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Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease Research Branch National Human Genome Reseach Institute, National Institutes of Health (NIH) Building: 49, Room 4A82 49 Convent Drive MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
     source          1. .741
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G270071A07"
                     /cell_type="melanocyte"
                     /clone_lib="RIKEN full-length enriched, melanocyte"
ORIGIN

  Query Match             13.0%;  Score 473.4;  DB 6;  Length 741;
  Best Local Similarity   89.3%;  Pred. No. 7.7e-120;
  Matches  510;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy       1320 AAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTT 1379
             | |||| |||||||| || |||||||||||||||||||||||||||| |||||||||||  ||
Db        171 AGATGACAGGTTGTATATCGTTATGGAGCTGATAGAAGGAGCCCCACTTGGAGAGCACTT 230

Qy       1380 CAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTAT 1439
              | |||||||||||||||||||||||||| | ||||||  |||| ||||||||||||||
Db        231 TAATTCTTTGAAGGAAAAACATCACCATTTCAGTGAAGAGCGACTGTGGAAAATATTTAT 290

Qy       1440 ACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCT 1499
              |||||||||||||||||||| ||   | ||||||||||||||||||| || ||||||||
Db        291 ACAGCTGTGCTTAGCTCTTCGGTATCTGCACAAGGAGAAGAGGATTGTTCACAGAGATCT 350

Qy       1500 GACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCT 1559
              || |||||||||||||| |||| |||||||||||||| || ||||||||||||||||||
Db        351 CACGCCAAACAACATTATGCTGGGAGATAAGGACAAAGTGACAGTTACTGACTTTGGCCT 410

Qy       1560 GGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTC 1619
              |||||||||||||| |||| |||||| || || ||| |||| ||||| ||||| |||||
Db        411 GGCAAAGCAAAAACAGGAAAGCAGTAAGCTTACATCTATGGTGGGAACGATCCTCTATTC 470

Qy       1620 TTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGG 1679
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Db        471 TTGCCCAGAGGTCCTGAAGAGTGAGCCATATGGAGAGAAGGCCGATGTCTGGGCTGCTGG 530

Qy       1680 CTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTC 1739
              |||||||||||||||||||||||||| | ||||| |||||||  ||||| |||||||| ||
Db        531 CTGCATCCTTTATCAGATGGCGACTCTAAGTCCTCCCTTCTGTAGCACCAACATGCTCTC 590

Qy       1740 CTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGA 1799
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Db        591 CTTGGCTACTAAAATAGTGGAGGCTGTATATGAGCCAGTGCCAGAAGGTATCTACTCTGA 650

Qy       1800 AAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATAT 1859
              |||||| ||||| ||||| || |||||||||||||||||| ||||| ||||||||||
Db        651 AAAAGTGACAGATACCATTAGAAGGTGCCTCACTCCTGATGCAGAAGCCCGTCCAGATAT 710

Qy       1860 TGTAGAAGTCAGTTCGATGATATCAGATGTC 1890
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Db        711 TGTAGAAGTTAGTTCCATGATATCAGATGTC 741
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```
RESULT 5
BM976126/c
LOCUS       BM976126                 664 bp    mRNA    linear   EST 21-FEB-2003
DEFINITION  UI-CF-EN1-acy-m-10-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-acy-m-10-0-UI 3', mRNA sequence.
ACCESSION   BM976126
VERSION     BM976126.1  GI:19593717
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            The following repetitive elements were found in this cDNA
            sequence: 1-48, >AT_rich#Low_complexity
            Seq primer: M13 FORWARD
            POLYA=Yes.
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                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
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TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"
ORIGIN

Query Match 12.6%; Score 457.4; DB 5; Length 664;
Best Local Similarity 99.8%; Pred. No. 2.1e-115;
Matches 458; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1224 AGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCA 1283
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Db        604 AGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCA 545

Qy       1284 TCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTAT 1343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         544 TCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTAT 485

Qy       1344 GGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCA 1403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 GGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCA 425

Qy       1404 CCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATA 1463
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Db         424 CCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATA 365

Qy       1464 CTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGG 1523
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Db         364 CTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGG 305

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Db         304 GGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAG 245

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Db         244 TAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTG 206
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RESULT 6
AI962584/c
LOCUS AI962584 523 bp mRNA linear EST 08-MAR-2000
DEFINITION wq54a01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2475048 3', mRNA sequence.
ACCESSION AI962584
VERSION AI962584.1 GI:5755297
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 523)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 695 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 454.
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/organism="Homo sapiens"
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/clone="IMAGE:2475048"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Query Match 12.1%; Score 441.2; DB 1; Length 523;
Best Local Similarity 99.3%; Pred. No. 6.4e-111;
Matches 443; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2890 ACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACT 2949
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         523 ACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACT 464

Qy       2950 GTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCAT 3009
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         463 GTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCAT 404

Qy       3010 TCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGT 3069
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         403 TCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGT 344

Qy       3070 GGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCC 3129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         343 GGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCC 284

Qy       3130 AAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGAC 3189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         283 AAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGAC 224

Qy       3190 TTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTG 3249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         223 TTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTG 164

Qy       3250 CCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTG 3309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         163 CCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTG 104

Qy       3310 CAAAATTCATCTTTTGGAGGATTGAG 3335
             ||||||||||||||||||| | | |
Db         103 CAAAATTCATCTTTTGGAGGGTGGGG 78
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RESULT 7
BU568655
LOCUS BU568655 831 bp mRNA linear EST 16-SEP-2002
DEFINITION AGENCOURT_10401740 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6615844 5', mRNA sequence.
ACCESSION BU568655
VERSION BU568655.1 GI:22918955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 831)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2858  row: j  column: 04
            High quality sequence start: 3
            High quality sequence stop: 322.
FEATURES             Location/Qualifiers
     source          1. .831
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6615844"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_82"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.35 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             11.7%;  Score 425;  DB 5;  Length 831;
  Best Local Similarity   86.9%;  Pred. No. 2.5e-106;
  Matches  569;  Conservative    0;  Mismatches   55;  Indels   31;  Gaps    8;

Qy        699 AAATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGA 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 AAATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGA 75

Qy        759 CACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTT 818
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         76 CACCAATGCCCACCAGGTGGTTCGGGAAAATGGTGTATATACAATAGCAAAATTAATTTT 135

Qy        819 ACCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAG--------GTAATAAAC 870
              |||||||||||||||||||||||||||||||||||||||||          |    | |
Db        136 ACCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGC 195

Qy        871 ATGTCTCTTGTCCTTCAGTAT-------------CAAGTTATTGAAATCTTGGGTAACTA 917
               |     ||   |||||||||             | | |  || |||   |      |
Db        196 CTTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCAC 255

Qy        918 TGACTTGTTTGAGATCTTCATTGACATA-GGGCATTATGTACGTGATATCAGTGCTTATG 976
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        256 AGACTTGTTTGAGATCTTCATTGACATAGGGGCATTATGTACGTGATATCAGTGCTTATG 315

Qy        977 AAG-AATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAA 1035
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAGAAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAA 375

Qy       1036 AATATTGAAAGCATTAATCAG-AACAAAGCTCCTTTGAAATATATAGGCAACTATGCAAT 1094
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        376 AATATTGAAAGCATTAATCAGAAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAAT 435

Qy       1095 TTTGGATCATCTTGGAAGTGGAGCTTTT--GGCTGTGTTTACAAGGTTAGAAAGCATAGT 1152
              |||||||||||||||||||||||||||  | ||||||||||||||||||||||||||||||
Db        436 TTTGGATCATCTTGGAAGTGGAGCTTTTTGGCTTGTGTTTACAAGGTTAGAAAGCATAGT 495

Qy       1153 GGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGAT 1212
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        496 GGTCAAAATCTTTTAGCAATGAAAGAAGTCAATTTACATAACCCAGCATTTGGGAAGGAT 555

Qy       1213 AAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTG-AATTAACAATAATTAAAGA 1271
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        556 AAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAAATTAACAATAATTAAAGA 615

Qy       1272 GCAGCTTT----ATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAA 1322
              ||||||||    ||   |   | |      |||||||||||||||   | |||
Db        616 GCAGCTTTTATCATTCCCAACATTTGTACGTTTATTACAAAACATTTTCTGGAAA 670


RESULT 8
AA954906/c
LOCUS       AA954906                508 bp    mRNA    linear   EST 07-JUL-1998
DEFINITION  op01b04.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1574383 3',
            mRNA sequence.
ACCESSION   AA954906
VERSION     AA954906.1  GI:3118601
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Stratagene, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 623    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 472.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1574383"
                     /sex="mixed"
                     /tissue_type="kidney tumor"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="NCI_CGAP_Kid6"
                     /note="Organ: kidney; Vector: Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
                     GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTTT 3' Average insert size:  1.0 kb."
ORIGIN

  Query Match             11.5%;  Score 418.2;  DB 1;  Length 508;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-104;
  Matches  420;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2912 AATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAAGAAGTCCTTGAGG 2971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 AATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAAGAAGTCCTTGAGG 449

Qy       2972 AAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCATGGGGGACCAAGA 3031
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        448 AAAGTGGCTATTACAATTNTACATCTAACAGGTATCATTCCTATCCATGGGGGACCAAGA 389

Qy       3032 ATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAGTGAAG 3091
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 ATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAGTGAAG 329

Qy       3092 TTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCTAGAGG 3151
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 TTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCTAGAGG 269

Qy       3152 GTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCTGTGCT 3211
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCTGTGCT 209

Qy       3212 GGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATATACAGGA 3271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATATACAGGA 149

Qy       3272 TGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCATCTTTTGGAGGAT 3331
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        148 TGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCATCTTTTGGAGGGT 89

Qy       3332 TGAG 3335
                | |
Db         88 GGGG 85


RESULT 9
AY404298
LOCUS       AY404298                441 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM1844 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY404298
VERSION     AY404298.1  GI:39760275
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 441)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .441
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>441
                     /locus_tag="HCM1844"
ORIGIN

  Query Match             11.4%;  Score 415;  DB 9;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-103;
  Matches  415;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 86

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 146

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 206

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 266

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 326

Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 386

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCAC 2037
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCAC 441


RESULT 10
BG717420
LOCUS       BG717420                682 bp    mRNA    linear   EST 08-MAY-2001
DEFINITION  602689765F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4821808 5',
            mRNA sequence.
ACCESSION   BG717420
VERSION     BG717420.1  GI:13996607
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 682)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10729  row: b  column: 17
            High quality sequence stop: 682.
FEATURES             Location/Qualifiers
     source          1. .682
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4821808"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_97"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             11.2%;  Score 407.4;  DB 4;  Length 682;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-101;
  Matches  419;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
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Db        261 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 320

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742

Db        321 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 380

Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802

Db        381 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAA 440

Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862

Db        441 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 500

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922

Db        501 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 560

Qy       1923 CCAGTTGTCCTTGGAA-AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTA 1981

Db        561 CCAGTTGTCCTTGGAACAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTA 620

Qy       1982 TGGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGA 2041

Db        621 TGGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGA 680

Qy       2042 C 2042

Db        681 C 681
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RESULT 11
BM976173/c
LOCUS       BM976173                 755 bp    mRNA    linear   EST 21-FEB-2003
DEFINITION  UI-CF-EN1-acy-e-15-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-acy-e-15-0-UI 3', mRNA sequence.
ACCESSION   BM976173
VERSION     BM976173.1  GI:19593764
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
             The following repetitive elements were found in this cDNA
            sequence: 1-48, >AT_rich#Low_complexity
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .755
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EN1-acy-e-15-0-UI"
                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-EN1
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN
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  Query Match             11.0%;  Score 401;  DB 5;  Length 755;
  Best Local Similarity   79.8%;  Pred. No. 1.2e-99;
  Matches  549;  Conservative    0;  Mismatches    1;  Indels  138;  Gaps    1;

Qy        935 TCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGC 994

Db        755 TCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGC 696

Qy        995 TGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATC 1054

Db        695 TGAATNTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATC 636

Qy       1055 AGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTG 1114

Db        635 AGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTG 576

Qy       1115 GAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGA 1174

Db        575 GAGCTTTTGGCTGTGTTTACA---------------------------------------- 555

Qy       1175 AAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCG 1234

Db        554 ---------------------------------------------------------- 555

Qy       1235 TAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTG 1294

Db        554 ----------------------------------------AGCTTTATCATCCCAACATTG 534

Qy       1295 TACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAG 1354

Db        533 TACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAG 474

Qy       1355 AAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTG 1414

Db        473 AAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTG 414

Qy       1415 AAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGG 1474

Db        413 AAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGG 354

Qy       1475 AGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACA 1534

Db        353 AGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACA 294

Qy       1535 AAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGT 1594
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Db        293 AAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGT 234

Qy       1595 CTGTGGTTGGAACAATCCTGTATTCTTG 1622
              ||||||||||||||||||||||||||||
Db        233 CTGTGGTTGGAACAATCCTGTATTCTTG 206


RESULT 12
AA889152/c
LOCUS       AA889152                464 bp    mRNA    linear   EST 04-JAN-1999
DEFINITION  ak25c10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406994
            3', mRNA sequence.
ACCESSION   AA889152
VERSION     AA889152.1  GI:3016031
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 464)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 953   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .464
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1406994"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares_testis_NHT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with  a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match            10.6%;  Score 385.2;  DB 1;  Length 464;
  Best Local Similarity   99.2%;  Pred. No. 2.5e-95;
  Matches  387;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2946 GACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTA 3005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTA 405

Qy       3006 TCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTT 3065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTT 345

Qy       3066 GAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGAT 3125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 GAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGAT 285

Qy       3126 GCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCA 3185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 GCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCA 225

Qy       3186 GGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTC 3245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTC 165

Qy       3246 ATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAAT 3305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 ATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAAT 105

Qy       3306 GCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
              |||||||||||||||||||||||||||||
Db        104 GCTGCAAAATTCATCTTTTGGAGGGTGGGG 75


RESULT 13
AA429606/c
LOCUS       AA429606                476 bp    mRNA    linear   EST 16-OCT-1997
DEFINITION  zw75f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782057
            3', mRNA sequence.
ACCESSION   AA429606
VERSION     AA429606.1  GI:2112707
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 454.
FEATURES             Location/Qualifiers
     source          1. .476
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:782057"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares_testis_NHT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with  a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match            10.5%;  Score 384;  DB 1;  Length 476;
  Best Local Similarity   98.7%;  Pred. No. 5.3e-95;
  Matches  387;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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Qy       2944 CAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGG 3003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGG 417

Qy       3004 TATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATT 3063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 TATCATTCCTATCCATGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATT 357

Qy       3064 TTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAG 3123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAG 297

Qy       3124 ATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTG 3183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 ATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTG 237

Qy       3184 CAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCT 3243
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        236 CAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGAATATGACAGCTGCGGTACTTGAGGGCT 177

Qy       3244 TCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAA 3303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 TCATTGCCAGAACACATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAA 117

Qy       3304 ATGCTGCAAAATTCATCTTTTGGAGGATTGAG 3335
             |||||||||| |||||||||||||| | | |
Db        116 ATGCTGCAAAACTCATCTTTTGGAGGGTGGGG 85
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RESULT 14
CR738506
LOCUS CR738506 472 bp mRNA linear EST 30-AUG-2004
DEFINITION CR738506 Soares_testis_NHT Homo sapiens cDNA clone IMAGp971E0777 ; IMAGE:1752177 5', mRNA sequence.
ACCESSION CR738506
VERSION CR738506.1 GI:51663301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 472)
AUTHORS Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E., Peters,M., Radelof,U. and Schneider,D.
TITLE I.M.A.G.E. cDNA Clone Collection
JOURNAL Unpublished (2004)
COMMENT Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGp971E0777.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1. .472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp971E0777 ; IMAGE:1752177"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares_testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Query Match 10.0%; Score 363.4; DB 7; Length 472;
Best Local Similarity 99.7%; Pred. No. 2.9e-89;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 167

Qy        979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 227

Qy       1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 287

Qy       1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 347

Qy       1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        348 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGGAAGGATAAGAAA 407

Qy       1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 467

Qy       1279 TATCA 1283
              |||||
Db        468 TATCA 472
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RESULT 15
BX722244
LOCUS BX722244 824 bp mRNA linear EST 18-NOV-2003
DEFINITION BX722244 XGC-tadpole Xenopus tropicalis cDNA clone TTpA072j13 5', mRNA sequence.
ACCESSION BX722244
VERSION BX722244.1 GI:38394985
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 824)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTpA072j13.p1kSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI

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           Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
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                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             9.3%;  Score 337.4;  DB 5;  Length 824;
  Best Local Similarity   66.1%;  Pred. No. 6.4e-82;
  Matches  532;  Conservative    0;  Mismatches  246;  Indels   27;  Gaps    2;

Qy        315 TCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTAACAGCGGAGTTGCT 374
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Db         20 TCTTATGATGATACTGCGTGAATTTGATCTTCTCTCCAAAAGGCTTGCAGCAGATCTCTT 79

Qy        375 GCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACC 434
              ||||| ||||||  |||||  |  | || ||||| || |||||  | | ||| ||  | ||
Db         80 ACGCCTTCTTTGTTCAGAGACAGAAGTAAAAGAACAAGTGAAAATTTTTGATGGTGTCCC 139

Qy        435 GGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGGAGCATTGTCTGGAT 494
              | | || ||||||||  ||||||||||  | ||| | || |||||  | ||||||||
Db        140 TACCTTACTTAGTCTGCTTCACTCTGACCATCTTAAGTTGCTTTGGAGTGTGGTCTGGAT 199

Qy        495 TCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGCATTTGGGGAGGCAT 554
              || || ||| ||||||||||  |||||  |  || || |||||  | |  |||||  || ||
Db        200 ACTTGTCCAGATTTGTGAGGATCCTGAAATAAGTGTTGAAATCAGAACATGGGGTGGAAT 259

Qy        555 CAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCTGATCACTCCTCCAT 614
              ||| ||||||  |  |||||||||  |  |||||      || |  | |||||||  |||||  |
Db        260 CAAGCAGCTTTTGCATATTTTAAAGGGAGAACAGTATCTAATCTCTGATCGTTCCTCTGT 319

Qy        615 TGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGA 674
              ||| || || || ||||||||||  | || || || |  || ||  |||||    |||||
Db        320 TGGGAGTCTATCAAGTGCAAATGCATCTGGACGTATTCGACATCTATATTTACATGAAGA 379

Qy        675 CTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGC 734
              |||||  ||  || ||||||||  |||||||    | |||||  ||  |||||||||||||||  ||
Db        380 TTTGAGTCCAAGTGAAATACAGGAAAATAAACTTTCACTCCAGGCAGCCTGCTGTGCAGC 439

Qy        735 CCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGT 794
              |||||  ||  ||  |||||  ||||||||  |||||  ||  ||  |  ||  ||||||||  |||||
Db        440 GCTCACAGAACTTGTGCTTAATGACACTAATGCTCATCAAATAGTACAGGAAAACGGTGT 499

Qy        795 ATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCAGCAAAAAGTAA--- 851
              ||  |  |||  |  ||  ||  ||||||||  |||||  |||  |   |  ||      ||  |||
Db        500 TTACATAATTGGAAGGTTGATTTTACCGAATAAACAACATGAATCAATTCGAAATAAGGC 559

Qy        852 -----------TCTATTACAGGTAATAAACATGTCTCTTGTCCTTCAGTAT--------- 891
                        |  ||||    |     | | |      ||  |  ||  ||  ||
Db        560 TTCTATATTGCAGTGTTACGCTTTCCGAGCTTTAAGGTTTTTGTTTAGCATGGAAAGAAA 619

Qy        892 ----CAAGTTATTGAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATTGACATAGG 947
                  |  ||  ||  |||   ||   |          |  | ||||||  |  ||  ||||||||  ||
Db        620 CAGGGATCTTTTTAAAAGATTTTTTCCACCAAATCTCTTTGAGGTGTTTATTGACATTGG 679

Qy        948 GCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAATTTATTAGT 1007
              |||||||  |  ||  |||||  |   ||  |||||  ||   |  |||    ||   |  ||  |    ||  |
Db        680 GCATTATATTCGGGATATTAAGGCATATGAGGATCTTGTACTTAAATTAAACTCTGTAAT 739

Qy       1008 GGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAACAAAGCTCC 1067
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Db        740 GGAAGCAGAACTTAAGCAAATTGCTGATAGTATTGAAAGCATCAATCAGAACAAAACGCC 799

Qy       1068 TTTGAAATATATAGGCAACTATGCA 1092
                |   ||||  ||||||  |||||||||
Db        800 TACAAAATTTATAGGAAACTATGCA 824


Search completed: May 12, 2005, 23:30:31
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2005, 18:14:59 ; Search time 10168 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2656.6	72.9	3919	6	AR562218	AR562218 Sequence
	2	2377.4	65.2	3348	6	AR562219	AR562219 Sequence
	3	2299.2	63.1	2562	6	AX250157	AX250157 Sequence
	4	1705	46.8	2043	6	AX714684	AX714684 Sequence
	5	1705	46.8	2043	9	AK057247	AK057247 Homo sapi
	6	1635	44.9	2037	9	BC045758	BC045758 Homo sapi
	7	1305.2	35.8	2638	6	CQ843340	CQ843340 Sequence
	8	1305.2	35.8	2638	9	AK123061	AK123061 Homo sapi
	9	1266.8	34.8	1601	9	AK098832	AK098832 Homo sapi
	10	1221.8	33.5	2097	9	HSM805951	BX537852 Homo sapi
	11	836.6	23.0	1812	6	CQ739715	CQ739715 Sequence
	12	599.6	16.5	1101	6	CQ739550	CQ739550 Sequence
	13	370.4	10.2	783	6	AX467416	AX467416 Sequence
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c	15	300.4	8.2	495	6	AX467419	AX467419 Sequence
	16	252	6.9	564	6	AR414537	AR414537 Sequence
	17	252	6.9	564	6	AX971371	AX971371 Sequence
	18	252	6.9	564	6	BD110090	BD110090 EST and e
c	19	227.8	6.3	163790	9	AC093555	AC093555 Homo sapi
	20	187.4	5.1	192	6	AX775544	AX775544 Sequence
	21	171	4.7	225154	2	AC106152	AC106152 Rattus no
c	22	171	4.7	315287	2	AC098988	AC098988 Rattus no
	23	169.8	4.7	210905	10	AC117608	AC117608 Mus muscu
	24	169.4	4.6	185100	10	AC129580	AC129580 Mus muscu
	25	163.4	4.5	269496	2	AC128462	AC128462 Rattus no
	26	126.4	3.5	667	6	AX467420	AX467420 Sequence
	27	104.8	2.9	400	6	CQ418817	CQ418817 Sequence
c	28	101.8	2.8	538	11	BV034140	BV034140 S212P6438
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	30	95.8	2.6	1551	10	BC019524	BC019524 Mus muscu
	31	95.8	2.6	2249	10	AF218847	AF218847 Mus muscu
c	32	95.8	2.6	40301	3	U00065	U00065 Caenorhabdi
	33	92.6	2.5	1314	10	AY334013	AY334013 Rattus no
c	34	89	2.4	274	11	G66873	G66873 G-107802 Ra
c	35	89	2.4	588	11	G55726	G55726 SHGC-100931
c	36	88	2.4	269496	2	AC128462	AC128462 Rattus no
	37	86.2	2.4	1852	8	BT000875	BT000875 Arabidops
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	43	79	2.2	906	6	AR130840	AR130840 Sequence
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ALIGNMENTS

RESULT 1
AR562218
LOCUS AR562218 3919 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6759222.
ACCESSION AR562218
VERSION AR562218.1 GI:53976128
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3919)
AUTHORS Meyers,R.E.
TITLE 14815, a human kinase family member and uses therefor
JOURNAL Patent: US 6759222-A 1 06-JUL-2004;
FEATURES Location/Qualifiers
source 1. .3919
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 72.9%; Score 2656.6; DB 6; Length 3919;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 2999; Conservative 0; Mismatches 39; Indels 279; Gaps 4;

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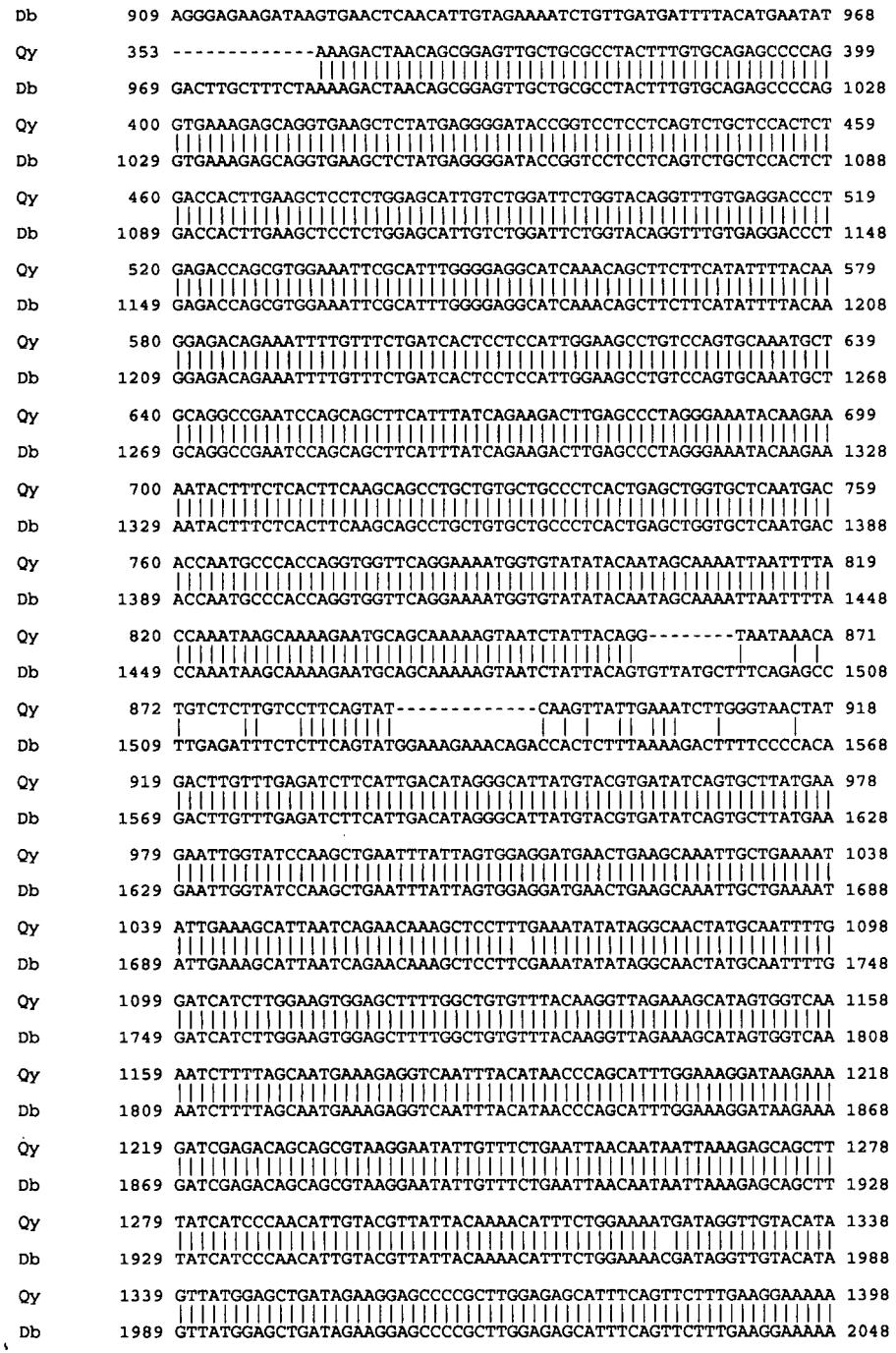
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Db 3009 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACC---------- 3049
Qy 2419 CTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGGCTGAG 2478
Db 3050 ---------- 3049

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Db       3050 ------------------------------------------------------------ 3049

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RESULT 2
AR562219
LOCUS       AR562219               3348 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 3 from patent US 6759222.
ACCESSION   AR562219
VERSION     AR562219.1  GI:53976129
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3348)
  AUTHORS   Meyers,R.E.
  TITLE     14815, a human kinase family member and uses therefor
  JOURNAL   Patent: US 6759222-A 3 06-JUL-2004;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             65.2%;  Score 2377.4;  DB 6;  Length 3348;
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  Matches 2718;  Conservative    0;  Mismatches   36;  Indels  279;  Gaps    4;

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Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
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Qy        353 ------------------------------------------------------------ 352

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Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
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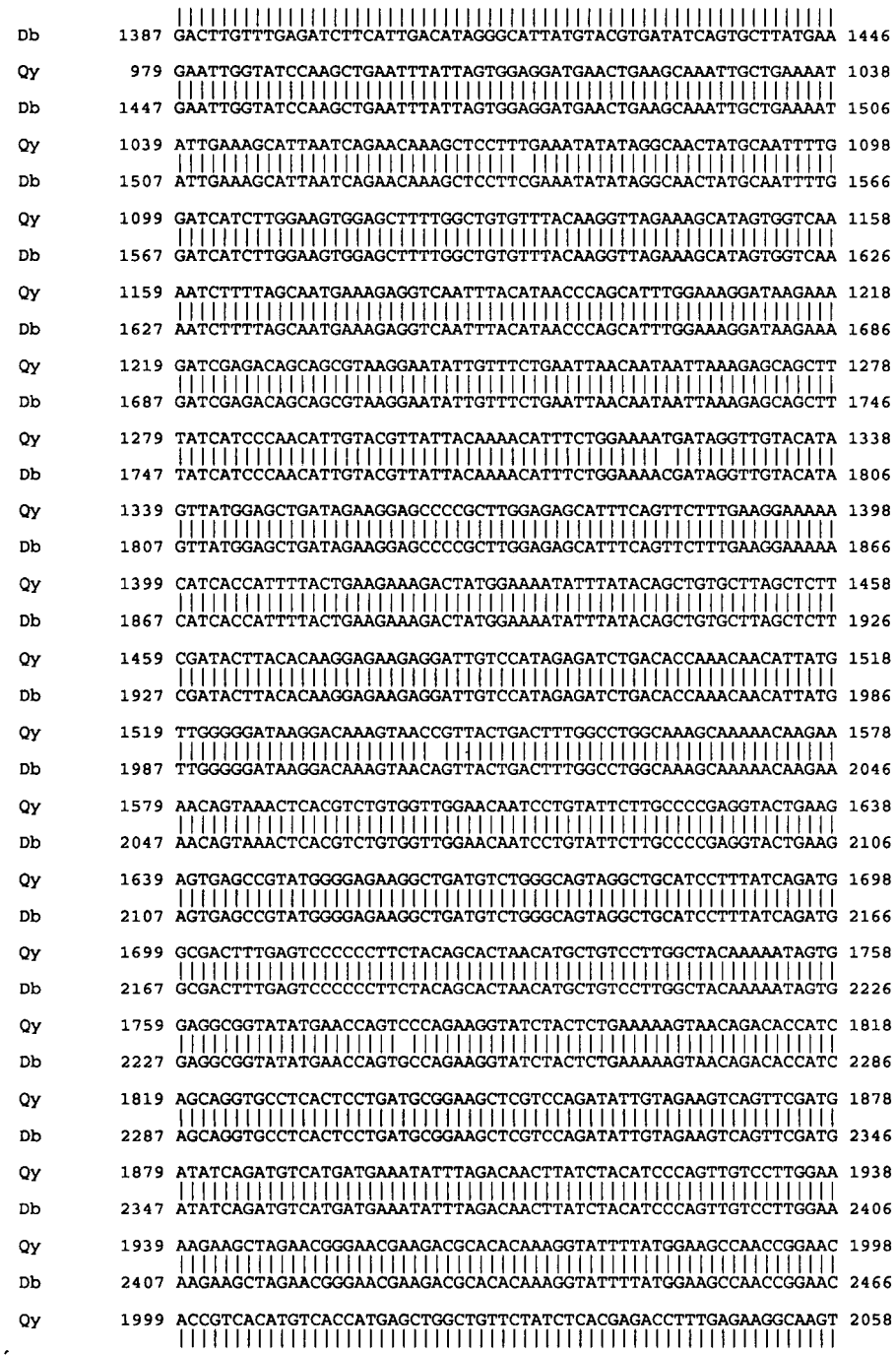
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Db 1867 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1926
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Db 3316 TGGGGGACCAAGAATCACCCAACCAAAAGATGA 3348

RESULT 3
AX250157

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DEFINITION  Sequence 2 from Patent WO0166594.
ACCESSION   AX250157
VERSION     AX250157.1  GI:15864532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G., Sudarsanam,S. and Martinez,R.
  TITLE     Human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0166594-A 2 13-SEP-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  97.6%;  Pred. No. 0;
  Matches 2363;  Conservative    0;  Mismatches   38;  Indels   21;  Gaps    2;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAGTATTATTTGATGAATCTGTTTTGCCACCTACAGTTTATTTTAAGAACTGCAGC 60

Qy         61 ATCTTGTTCCTTGCTTCCTTGGGTGCTTTTGGTGTCCTGACTGGCTTGTTGGTTTGGTCC 120
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
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Qy        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180
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Db        121 TTCATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCAC 180

Qy        181 ACTGTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGAT 240
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Qy        241 CAAAGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCC 300
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Qy        301 CGAGATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGACTA 360
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Qy        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420
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Db        361 ACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAGGTGAAAGAGCAGGTGAAGCTC 420

Qy        421 TATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCTGACCACTTGAAGCTCCTCTGG 480
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Qy        481 AGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCTGAGACCAGCGTGGAAATTCGC 540
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Db        541 ATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAAGGAGACAGAAATTTTGTTTCT 600

Qy        601 GATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCTGCAGGCCGAATCCAGCAGCTT 660
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Qy        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720
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Db        661 CATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAAAATACTTTCTCACTTCAAGCA 720

Qy        721 GCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGACACCAATGCCCACCAGGTGGTT 780
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Qy        781 CAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTACCAAATAAGCAAAAGAATGCA 840
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Qy        841 GCAAAAAGTAATCTATTACAG--------GTAATAAACATGTCTCTTGTCCTTCAGTAT- 891
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Qy        892 ------------CAAGTTATTGAAATCTTGGGTAACTATGACTTGTTTGAGATCTTCATT 939
                         | | |  || |||  |     |  |||||||||||||||||||||
Db        901 GAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACAGACTTGTTTGAGATCTTCATT 960

Qy        940 GACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTGAAT 999
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Qy       1000 TTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAGAAC 1059
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Qy       1060 AAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGAGCT 1119
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Qy       1120 TTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAAGAG 1179
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Qy       1180 GTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTAAGG 1239
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Qy       1240 AATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGT 1299
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Qy       1300 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1359
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Db       1321 TATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGA 1380

Qy       1360 GCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAA 1419
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Qy       1420 AGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAG 1479
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Qy       1960 AGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCATGAG 2019
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Qy       2080 GCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAG 2139
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AX714684
LOCUS       AX714684               2043 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 1368 from Patent EP1293569.
ACCESSION   AX714684
VERSION     AX714684.1  GI:29889637
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNAs
  JOURNAL   Patent: EP 1293569-A 1368 19-MAR-2003;
            Helix Research Institute (JP) ; Research Association for
            Biotechnology (JP)
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ORIGIN

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Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
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Qy       1923 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 1982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTAT 615

Qy       1983 GGAAGCCAACCGGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGAC 2042
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Qy       2043 CTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACT 2102
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Qy       2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
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Qy       2163 CAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGA 2222
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Qy       2523 TCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGG 2582
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Qy       2643 TCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAA 2702
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RESULT 5
AK057247
LOCUS AK057247 2043 bp mRNA linear PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ32685 fis, clone TESTI2000154, weakly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III (EC 2.7.1.-).
ACCESSION AK057247
VERSION AK057247.1 GI:16552861
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039
REFERENCE 2
AUTHORS Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S., Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2043)
AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

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                     GAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDEL
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                     RKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLKS
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ORIGIN
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Query Match 46.8%; Score 1705; DB 9; Length 2043;
Best Local Similarity 99.7%; Pred. No. 0;

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Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
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Db        256 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 315

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
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Db        316 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 375

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Db        856 TACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTC 915

Qy       2283 AAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGG 2342
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RESULT 6
BC045758
LOCUS       BC045758               2037 bp    mRNA    linear   PRI 07-OCT-2003
DEFINITION  Homo sapiens hypothetical protein FLJ32685, mRNA (cDNA clone
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ACCESSION   BC045758
VERSION     BC045758.1  GI:28279061
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2037)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2037)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 90 Row: f Column: 1
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 22749114.
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Qy      1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATC 1922
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Qy      2103 TTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGA 2162
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Qy      2343 AGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGC 2402
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Qy      2463 GGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCT 2522
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Qy       2883 TGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGAT 2942
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Qy       3123 GATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCT 3182
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DEFINITION  Sequence 1987 from Patent EP1440981.
ACCESSION   CQ843340
VERSION     CQ843340.1  GI:50895127
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
  TITLE     Full-length human cdna
  JOURNAL   Patent: EP 1440981-A 1987 28-JUL-2004;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
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Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
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Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
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Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
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Qy        353 ------------------------------------------------------------ 352
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Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
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Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
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Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
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Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
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Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
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Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
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Qy       1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
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Qy       1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
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RESULT 8
AK123061

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LOCUS       AK123061                2638 bp    mRNA    linear   PRI 09-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ41066 fis, clone TRACH2009310, weakly similar
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ACCESSION   AK123061
VERSION     AK123061.1  GI:34528519
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,
            Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K.,
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            Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A.,
            Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.
            and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2638)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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            Evaluation; clone selection for full insert sequencing: HRI and
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  Matches 1463;  Conservative    0;  Mismatches   33;  Indels  108;  Gaps    3;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 820

Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 880

Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 940

Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG---------------- 352
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 1000

Qy        353 ------------------------------------------------------------ 352

Db       1001 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 1060

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 1120

Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 1180

Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
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Db       1181 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 1240

Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 1300

Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
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Db       1301 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 1360

Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 1420

Qy        700 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 759
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Db       1421 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 1480

Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1481 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 1540

Qy        820 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAG--------GTAATAAACA 871
              ||||||||||||||||||||||||||||||||||||||||||        |  | |
Db       1541 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCC 1600

Qy        872 TGTCTCTTGTCCTTCAGTAT-------------CAAGTTATTGAAATCTTGGGTAACTAT 918
              |     ||   |||||||||             | | |  || |||   |      |
Db       1601 TTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACA 1660

Qy        919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 1720

Qy        979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
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Db       1721 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1780

Qy       1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
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Db       1781 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1840

Qy       1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1841 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1900

Qy       1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1901 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGGAAGGATAAGAAA 1960

Qy       1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1961 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 2020

Qy       1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
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Db       2021 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 2080

Qy       1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
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Db       2081 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 2140

Qy       1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2141 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 2200

Qy       1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2201 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 2260

Qy       1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2261 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 2320

Qy       1579 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTG 1622
              |||||||||||||||||||||||||||||||||||||||||||
Db       2321 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTG 2364
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RESULT 9
AK098832

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LOCUS       AK098832               1601 bp    mRNA    linear   PRI 12-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ25966 fis, clone TST05207.
ACCESSION   AK098832
VERSION     AK098832.1  GI:21758965
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Suzuki,Y., Hata,H.,
            Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T.,
            Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A.,
            Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1601)
  AUTHORS   Sugano,S. and Suzuki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction and 5'-end one pass sequencing: Institute of Medical
            Science, University of Tokyo, Laboratory of Genome Structure, Human
            Genome Center; 3'-end one pass sequencing: RAB; clone selection for
            full insert sequencing: RAB and Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="TST05207"
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                     NTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRA
                     CDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG
                     ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAV
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ORIGIN

  Query Match           34.8%;  Score 1266.8;  DB 9;  Length 1601;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1268;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1274 AGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGT 1333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGCTTTATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGT 197

Qy       1334 ACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGG 1393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 ACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGG 257

Qy       1394 AAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAG 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 AAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAG 317

Qy       1454 CTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACA 1513
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Db        318 CTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACA 377

Qy       1514 TTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAAC 1573

Db        378 TTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAAC 437

Qy       1574 AAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTAC 1633

Db        438 AAGAAAACAGTAAACTCACCTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTAC 497

Qy       1634 TGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATC 1693

Db        498 TGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATC 557

Qy       1694 AGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAA 1753

Db        558 AGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAA 617

Qy       1754 TAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACA 1813

Db        618 TAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACA 677

Qy       1814 CCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTT 1873

Db        678 CCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTT 737

Qy       1874 CGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCT 1933

Db        738 CGATGATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCT 797

Qy       1934 TGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACC 1993

Db        798 TGGAAAAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACC 857

Qy       1994 GGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGG 2053

Db        858 GGAACACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGG 917

Qy       2054 CAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCG 2113

Db        918 CAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCG 977

Qy       2114 CAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTG 2173

Db        978 CAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTG 1037

Qy       2174 ACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAG 2233

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Qy       2294 AAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAAT 2353

Db       1158 AAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAAT 1217

Qy       2354 CCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTC 2413

Db       1218 CCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTC 1277

Qy       2414 TTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGG 2473

Db       1278 TTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGG 1337

Qy       2474 CTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCA 2533

Db       1338 CTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCA 1397

Qy       2534 AAGATCATGG 2543
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Db       1398 AAGATCATGG 1407


RESULT 10
HSM805951
LOCUS       HSM805951              2097 bp    mRNA    linear   PRI 17-JUN-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp779L2259 (from clone DKFZp779L2259).
ACCESSION   BX537852
VERSION     BX537852.1  GI:31873839
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2097)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            This clone (DKFZp779L2259) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           33.5%;  Score 1221.8;  DB 9;  Length 2097;
  Best Local Similarity   90.2%;  Pred. No. 0;
  Matches 1385;  Conservative    0;  Mismatches   42;  Indels  108;  Gaps    3;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
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Db        267 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 326
Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
Db        327 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 386
Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
Db        387 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 446
Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
Db        447 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAGGTCAAGAATGT 506
Qy        353 ---------------------------------------------------------- 352
Db        507 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 566
Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
Db        567 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 626
Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
Db        627 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 686
Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
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Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
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Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
Db        807 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 866
Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
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Qy        700 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 759
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Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
Db        987 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 1046
Qy        820 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAG--------GTAATAAACA 871
Db       1047 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCC 1106
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Qy       1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
Db       1287 ATTGAAAGCATTAATCAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTG 1346
Qy       1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
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Qy       1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
Db       1407 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1466
Qy       1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
Db       1467 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1526
Qy       1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
Db       1527 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATA 1586
Qy       1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
Db       1587 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1646
Qy       1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
Db       1647 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1706
Qy       1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
Db       1707 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1766
Qy       1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTT 1553
Db       1767 TTGGGGGATAAGGACAAAGTAACAGTTAGTTGTTT 1801
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RESULT 11
CQ739715
LOCUS CQ739715 1812 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 25649 from Patent WO02068579.
ACCESSION CQ739715
VERSION CQ739715.1 GI:42343469
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 25649 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1. .1812
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 23.0%; Score 836.6; DB 6; Length 1812;
Best Local Similarity 69.2%; Pred. No. 1.3e-216;
Matches 1395; Conservative 0; Mismatches 329; Indels 291; Gaps 7;

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Qy        124 ATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACT 183
Db          1 ATGCAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACT 60
Qy        184 GTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAA 243
Db         61 GTGGACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAA 120
Qy        244 AGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGA 303
Db        121 AGAGAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGA 180
Qy        304 GATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG---------- 352
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Db        181 GATACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAA 240
Qy        353 ------------------------------------------------------------ 352
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Qy        353 ----------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCC 396
                              ||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATGACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCC 360
Qy        397 CAGGTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCAC 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCAC 420
Qy        457 TCTGACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGAC 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGAC 480
Qy        517 CCTGAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTA 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTGAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTA 540
Qy        577 CAAGGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAAT 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAGGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAAT 600
Qy        637 GCTGCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAA 696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTGCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAA 660
Qy        697 GAAAATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAAT 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAAT 720
Qy        757 GACACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATT 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATT 780
Qy        817 TTACCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGGTAATAAACATGTCT 876
              ||||||||||||||||||||||||||||||||||||||||||| | |||
Db        781 TTACCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGGTTAGAAA------- 833
Qy        877 CTTGTCCTTCAGTATCAAGTTATTGAAATCTTGGGTAACTATGACTTGTTTGAGATCTTC 936
                  | |    ||||  | ||  |    ||    |    | ||   | |
Db        834 -----GCATAGTGGTCAAAATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCA 888
Qy        937 ATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAAGAATTGGTATCCAAGCTG 996
              |||  |  |   |  | |  || || | |||  |      |     |
Db        889 TTTGGGAAGGATAAGAAAGATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACA 948
Qy        997 AATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAATATTGAAAGCATTAATCAG 1056
              |   |   || | ||||| ||     |   ||  | ||| || |||||   | | ||  ||
Db        949 ATAATTAAAGAGCAGGATCAAACTGATGGAAAGGATGATAACATTGAGTCCTTAAAGGAG 1008
Qy       1057 AACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTGGATCATCTTGGAAGTGGA 1116
               |   ||   |    | |   | |   ||    || |   ||||
Db       1009 GAGGTAGTGGCAGGCAGAAGCAAAACAAATGGGGCTAGAATGGA---------------- 1052
Qy       1117 GCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAAAATCTTTTAGCAATGAAA 1176
Db       1053 ------------------------------------------------------------ 1052
Qy       1177 GAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAAGATCGAGACAGCAGCGTA 1236
                ||  ||| | || | || |||||   ||||    |    |.||  ||
Db       1053 -GAGTACATTAAGATTAACCTGCATTAACAAAGAGGATCCCAAATGCAG----------- 1100
Qy       1237 AGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTA 1296
                                          |||||| |    |  |    |  |  |
Db       1101 ----------------------GTGCTTAGAAAGAGGACTCACAGTACAGTGGGTTATTT 1138
Qy       1297 CGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAA 1356
              |  | | ||  |||| | |   |          |  |    |     || | |||  | |
Db       1139 CTCTTTCACGGAACAATCCCAAATGCATTGTCTTCATCTGTGTGGTTGAAACTGCCATAG 1198

Qy       1357 GGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAA 1416
                |  | | |  | ||| ||| |   | |  ||||||| | | | | |||     | |
Db       1199 CCATGCTCACATCCA-AGCCTTTGAAACCATCCAAGGAAACAGACCCCGATTCAGTGGTA 1257
Qy       1417 GAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAG 1476
                | |  |                 ||  || | |  ||    | | ||| ||||||
Db       1258 CATGGGGAA----------------AGTCATGATGTGGGTTTTTCCAATGACAGAAGGAG 1301
Qy       1477 AAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAA 1536
              ||||| ||     | || |     |  |  |     ||  |     | || | |  |
Db       1302 AAGAGAATGTGAAAAAGGGGCTCAATTCAGCAGTTATTTGGGACCTAGAATTAAAAAGAT 1361
Qy       1537 GTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCT 1596
                | |  | | | |
Db       1362 TTGTCGGCCAGTTA---------------------------------------------- 1375
Qy       1597 GTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAG 1656
                                 ||     ||||||||||||||||||||||||||||||||
Db       1376 -------------------ATGAGATCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAG 1416
Qy       1657 AAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCC 1716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 AAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCC 1476
Qy       1717 TTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCA 1776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 TTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCA 1536
Qy       1777 GTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCT 1836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 GTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCT 1596
Qy       1837 GATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATG 1896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 GATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATGATATCAGATGTCATGATG 1656
Qy       1897 AAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAA 1956
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 AAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAAAAGAAGCTAGAACGGGAA 1716
Qy       1957 CGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCAT 2016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 CGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAACACCGTCACATGTCACCAT 1776
Qy       2017 GAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAA 2051
              ||||||||||||||||||    |  ||  || |
Db       1777 GAGCTGGCTGTTCTATCTCACATTATTTTGAAGTA 1811
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RESULT 12
CQ739550
LOCUS       CQ739550               1101 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 25484 from Patent WO02068579.
ACCESSION   CQ739550
VERSION     CQ739550.1  GI:42342854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 25484 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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ORIGIN

  Query Match            16.5%;  Score 599.6;  DB 6;  Length 1101;
  Best Local Similarity  82.5%;  Pred. No. 6.2e-152;
  Matches  805;  Conservative    0;  Mismatches   39;  Indels  132;  Gaps    5;

Qy       2038 GAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGT 2097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGACCTTTGAGAAGGCAAGTTTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGT 60

Qy       2098 GAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGAC 2157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAACTTTCAGAAAGCGCAGACCTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGAC 120

Qy       2158 GAAGACAGGGCCTGTGACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAG 2217
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGACAGGGCCTGTAACGAAATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAG 180

Qy       2218 AAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCC 2277
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGATACATATTCAGAGGTAGATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCC 240

Qy       2278 AGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCA 2337
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        241 AGTTCAAGCCCTCTGAAAGAATCTACATTCAACATTTTAAAGAGAAGTTTTAGTGC-TCA 299

Qy       2338 GGAGGAGAAAGACAATCCCAAACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGA 2397
             ||||||||||||||||||||||||
Db        300 GGAGGAGAAAGACAATCCCAAACAAG---------------------------------- 325

Qy       2398 CCAGCTTTGCTGCCTCTTGACCTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCAC 2457
                                       || |||||  | |   | ||||
Db        326 ----------------------TGTTTCTGGGAATAAAAACCCA---------------- 347

Qy       2458 ATTAAGGAAATAGAGGCTGAGTTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTG 2517
                      |||   | |||   ||||||||
Db        348 -------------AGGAAAACTTATCAACAGGGTG------------------------- 369

Qy       2518 ATTCTTCGAAATCTCAAAGATCATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCA 2577
                | |     |||  ||||||  | |   | |                  |   |||||
Db        370 --TATGATCTATCAGAAAGATATTCGATAAAA------------------CCCTCATCA 408

Qy       2578 GCAGGAATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATA 2637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 GCAGGAATTGCTGTGTCCCAGAGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATA 468

Qy       2638 TTAATTCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAAT 2697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTAATTCAGCTGCACAAAATAATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAAT 528

Qy       2698 TTGAAAAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCT 2757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 TTGAAAAGAAGGGTTATAGAGAGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCT 588

Qy       2758 TGTAATTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 TGTAATTTGAAATCTGAAATTAAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCC 648

Qy       2818 AACTTTTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCC 2877
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Db        649 AACTTTTTCACAGCAGATTACCATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCC 708

Qy       2878 CCAAATGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAA 2937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 CCAAATGACCCTACAGGTTTACCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAA 768

Qy       2938 CAGATGCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCT 2997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 CAGATGCAGACTGTGATTGAAGAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCT 828

Qy       2998 AACAGGTATCATTCCT 3013
             ||||| | |  || ||
Db        829 AACAGATGTAGTTGCT 844
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RESULT 13
AX467416
LOCUS       AX467416                783 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 1 from Patent WO0233095.
ACCESSION   AX467416
VERSION     AX467416.1  GI:21900624
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Smolyar,A.
  TITLE     Regulation of human serine-threonine protein kinase
  JOURNAL   Patent: WO 0233095-A 1 25-APR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            10.2%;  Score 370.4;  DB 6;  Length 783;
  Best Local Similarity  84.8%;  Pred. No. 2.3e-89;
  Matches  451;  Conservative    0;  Mismatches   51;  Indels   30;  Gaps    2;

Qy       1320 AAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTT 1379
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 AGATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTT 311

Qy       1380 CAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTAT 1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 CAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTAT 371

Qy       1440 ACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCT 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 ACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCA 431

Qy       1500 GACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCT 1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTAGCAGCTTTGGTGA 491

Qy       1560 GGCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTC 1619
                 ||||||    |  | | ||  |              |   ||  ||  |||
Db        492 TCTCCAGCAAATGGGTGTGGAAATTATGTTGCGAAACACATCCCAACATATTTTGCCTTC 551

Qy       1620 ---------TTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTG 1670
                      || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GCAGAAAATTTTCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTG 611

Qy       1671 GGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAA 1730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 GGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAA 671

Qy       1731 CATGCTGTCCTTGGCTACAAAAATA--------------------GTGGAGGCGGTATA 1769
             |||||||||||||||||||||||| ||                    ||||||||||||||
Db        672 CATGCTGTCCTTGGCTACAAAAGTAAGCAACGCTGGGAGACAGAAGGTGGAGGCGGTATA 731

Qy       1770 TGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGC 1821
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 TGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGC 783
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RESULT 14
AC098931/c
LOCUS       AC098931              179082 bp    DNA     linear   PRI 18-DEC-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-353I6, complete sequence.
ACCESSION   AC098931 AC069203
VERSION     AC098931.3  GI:27228862
KEYWORDS    HTG.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 179082)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 179082)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 179082)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 4 (bases 1 to 179082)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
COMMENT On Dec 18, 2002 this sequence version replaced gi:18921334.
---------- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: WUGSC
---------- Project Information
Center project name: chr-3
Center clone name: RP11-353I6 (bc0381)
---------- Summary Statistics
Sequencing vector: plasmid; L08752; 24% of reads
Sequencing vector: plasmid; 38% of reads
Sequencing vector: M13; 38% of reads
Chemistry: Dye-terminator ET; 21% of reads
Chemistry: Dye-terminator Big Dye; 41% of reads
Chemistry: Dye-primer ET; 38% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179061 bases at least Q40
Consensus quality: 179079 bases at least Q30
Consensus quality: 179082 bases at least Q20
Insert size: 179082; sum-of-contigs
Quality coverage: 10.8x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-130I17 (UWGC:bc0249) AC093558, 22996-bp overlap
3': RP11-30A19 (UWGC:bc0147) AC093555, 3298-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BglII		EcoRI		HindIII	
SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt
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4899	5132	3599	3563	512	<800
243	<800	8653	8739	449	<800
818	898	315	<800	1596	1550
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763	726	415	<800	499	<800
949	898	5321	5190	288	<800
578	<800	893	932	2352	2406
5515	5582	4414	4568	654	<800
2713	2785	5296	5190	2876	2892
4074	4085	933	932	191	<800
424	<800	6197	6116	5412	5326
1572	1515	169	<800	928	967
8471	8538	846	932	6163	6585
283	<800	2814	2846	1826	1823
3744	3752	187	<800	103	<800
10843	10519	1075	1071	2182	2105
1879	1892	2405	2354	799	824
2459	2510	1438	1411	2074	1950
133	<800	4121	4177	11718	11359
897	898	1802	1799	1561	1550
7822	7827	3628	3563	1951	1950

7362	7373	2613	2719	8017	8018
896	898	126	<800	323	<800
479	<800	3024	3056	123	<800
729	726	726	<800	3469	3534
1289	1268	2057	2138	1558	1550
29957	30037	2102	2138	5614	5594
9257	9354	10228	10234	1881	1859
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3188	3228	933	932	270	<800
1922	1892	4215	4177	471	<800
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5604	5582	1155	1177	6641	6585
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10701	10519	1554	1494	6657	6585
8544	8538	2415	2505	1130	1135
3302	3228	5376	5190	11402	11359
6115	6210	2351	2354	3514	3534
710	<800	2169	2354	130	<800
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Query Match 9.3%; Score 338; DB 9; Length 179082;
Best Local Similarity 97.2%; Pred. No. 3.9e-80;
Matches 344; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       3042 CAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGATTTTCTCAGTGAAGTTCAAGTTCT 3101
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Qy       3102 GGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGGGTGCTGCTAGAGGGTGTGGAAAA 3161
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Qy       3162 GACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTGGGGGTCCTGTGCTGGAGTATATG 3221
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Qy       3222 ACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACACATTATATACAGGATGTCAGAGCT 3281
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RESULT 15
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LOCUS AX467419 495 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 4 from Patent WO0233095.
ACCESSION AX467419
VERSION AX467419.1 GI:21900625
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Smolyar,A.
TITLE Regulation of human serine-threonine protein kinase
JOURNAL Patent: WO 0233095-A 4 25-APR-2002;
Bayer Aktiengesellschaft (DE)
FEATURES Location/Qualifiers
source 1. .495
/organism="Homo sapiens"
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ORIGIN

Query Match 8.2%; Score 300.4; DB 6; Length 495;
Best Local Similarity 99.7%; Pred. No. 2.9e-70;
Matches 301; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        495 AATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTC 436

Qy       1381 AGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATA 1440
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Qy       1441 CAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTG 1500
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Db        375 CAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTG 316

Qy       1501 ACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTG 1560
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Db        315 ACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTG 256

Qy       1561 GCAAAGCAAAAACAAGAAAACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCT 1620
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Qy       1621 TG 1622
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2005, 18:17:24 ; Search time 407 Seconds
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Title: PCT-US03-32302-1
Perfect score: 3644
Sequence: 1 atgagagtattatttgatga.....acccatgcggaatccactag 3644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2656.6	72.9	3919	4	US-10-335-711-1	Sequence 1, Appli
2	2377.4	65.2	3348	4	US-10-335-711-3	Sequence 3, Appli
3	252	6.9	564	4	US-09-621-976-2174	Sequence 2174, Ap
4	79	2.2	906	3	US-09-221-235-3	Sequence 3, Appli
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6	79	2.2	906	3	US-09-221-527-3	Sequence 3, Appli
7	79	2.2	906	3	US-09-221-236-3	Sequence 3, Appli
8	79	2.2	906	3	US-09-221-416-3	Sequence 3, Appli
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16	79	2.2	4137	3	US-09-221-928-1	Sequence 1, Appli
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18	79	2.2	4137	3	US-09-221-236-1	Sequence 1, Appli
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26	76.2	2.1	1582	4	US-09-949-016-3834	Sequence 3834, Ap
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45	60.8	1.7	1392	4	US-09-023-655-953	Sequence 953, App

ALIGNMENTS

RESULT 1
US-10-335-711-1
; Sequence 1, Application US/10335711
; Patent No. 6759222
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 14815, A Human Kinase Family Member and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: MPI02-002P1RNM
; CURRENT APPLICATION NUMBER: US/10/335,711
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/345,853
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3919
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)...(3530)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3899
; OTHER INFORMATION: n=a, c, g, or g
US-10-335-711-1

Query Match 72.9%; Score 2656.6; DB 4; Length 3919;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 2999; Conservative 0; Mismatches 39; Indels 279; Gaps 4;

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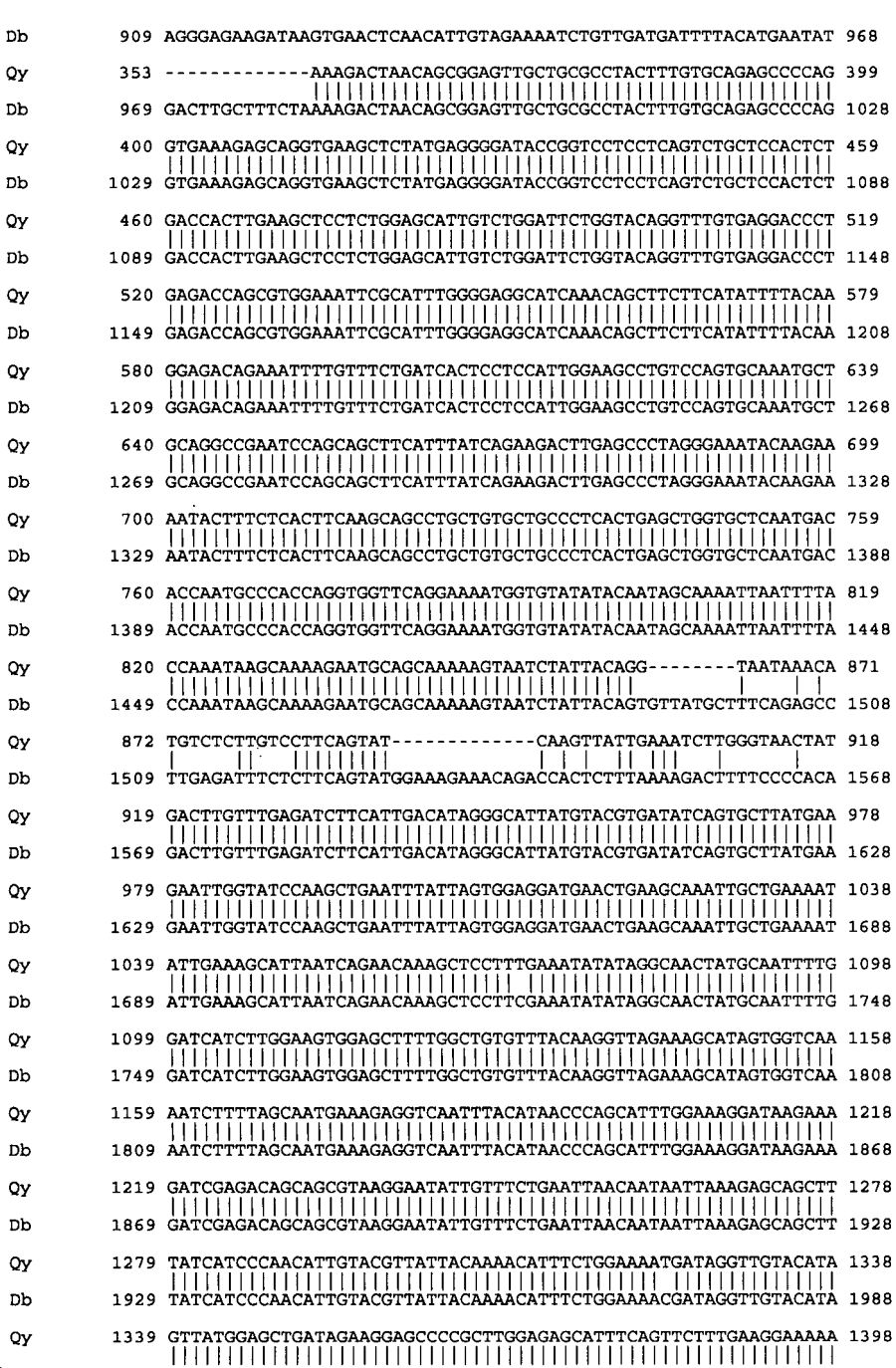
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Db 3050 ---------- 3049

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Qy       2479 TTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCAAAGAT 2538
Db       3050 ------------------------------------------------------------ 3049

Qy       2539 CATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGGAATTGCTGTGTCCCAG 2598
                                                 ||||||||||||||||||||||||||
Db       3050 ------------------------------AGCATCAGCAGGAATTGCTGTGTCCCAG 3077

Qy       2599 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3078 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 3137

Qy       2659 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 2718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3138 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 3197

Qy       2719 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 2778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3198 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 3257

Qy       2779 AAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTAC 2838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3258 AAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTAC 3317

Qy       2839 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 2898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3318 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 3377

Qy       2899 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 2958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3378 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 3437

Qy       2959 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3438 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3497

Qy       3019 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3498 TGGGGGACCAAGAATCACCCAACCAAAAGATGAAAATGCTGCATTTTGAGTGGACTTGAT 3557

Qy       3079 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3558 TTTCTCAGTGAAGTTCAAGTTCTGGACTTCAGCCGCTATTGCAAGATGCCCAAGGATTGG 3617

Qy       3139 GTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTG 3198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3618 GTGCTGCTAGAGGGTGTGGAAAAGACCAAGATGCCATGGGGCCTGCAGGACTTCTTTCTG 3677

Qy       3199 GGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACAC 3258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3678 GGGGTCCTGTGCTGGAGTATATGACAGCTGCGGTACTTGAGGGCTTCATTGCCAGAACAC 3737

Qy       3259 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3318
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Db       3738 ATTATATACAGGATGTCAGAGCTACCAGTGTGCTGCTGGGAGAAAATGCTGCAAAATTCA 3797

Qy       3319 TCTTTTGGAGGATTGAG 3335
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Db       3798 TCTTTTGGAGGGTGGGG 3814
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RESULT 2
US-10-335-711-3
; Sequence 3, Application US/10335711
; Patent No. 6759222
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel E.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 14815, A Human Kinase Family Member and
;  TITLE OF INVENTION:  Uses Therefor
;  FILE REFERENCE: MPI02-002P1RNM
;  CURRENT APPLICATION NUMBER: US/10/335,711
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: 60/345,853
;  PRIOR FILING DATE: 2002-01-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3348
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(3348)
US-10-335-711-3

  Query Match           65.2%;  Score 2377.4;  DB 4;  Length 3348;
  Best Local Similarity  89.6%;  Pred. No. 0;
  Matches 2718;  Conservative    0;  Mismatches   36;  Indels  279;  Gaps    4;

Qy        127 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 186
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Db        487 CAGTATATGGAGATTGTAGCCAATGAGTACCTCGGCTATGGAGAAGAGCAGCACACTGTG 546

Qy        187 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAAGCTGGTCAACATGACATATATTTTTCAAAAACTTGCTGCAGTCAAAGATCAAAGA 606

Qy        247 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GAATGGGTCACCACAAGTGGAGCCCACAAGACATTAGTAAATTTACTTGGTGCCCGAGAT 666

Qy        307 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAG-------------- 352
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        667 ACTAATGTTCTATTGGGTTCCCTTCTGGCTCTGGCTAGTTTAGCAGAAAGTCAAGAATGT 726

Qy        353 ------------------------------------------------------------ 352
Db        727 AGGGAGAAGATAAGTGAACTCAACATTGTAGAAAATCTGTTGATGATTTTACATGAATAT 786

Qy        353 -------------AAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 399
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GACTTGCTTTCTAAAAGACTAACAGCGGAGTTGCTGCGCCTACTTTGTGCAGAGCCCCAG 846

Qy        400 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 GTGAAAGAGCAGGTGAAGCTCTATGAGGGGATACCGGTCCTCCTCAGTCTGCTCCACTCT 906

Qy        460 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GACCACTTGAAGCTCCTCTGGAGCATTGTCTGGATTCTGGTACAGGTTTGTGAGGACCCT 966

Qy        520 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GAGACCAGCGTGGAAATTCGCATTTGGGGAGGCATCAAACAGCTTCTTCATATTTTACAA 1026

Qy        580 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GGAGACAGAAATTTTGTTTCTGATCACTCCTCCATTGGAAGCCTGTCCAGTGCAAATGCT 1086

Qy        640 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GCAGGCCGAATCCAGCAGCTTCATTTATCAGAAGACTTGAGCCCTAGGGAAATACAAGAA 1146

Qy        700 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 AATACTTTCTCACTTCAAGCAGCCTGCTGTGCTGCCCTCACTGAGCTGGTGCTCAATGAC 1206

Qy        760 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 ACCAATGCCCACCAGGTGGTTCAGGAAAATGGTGTATATACAATAGCAAAATTAATTTTA 1266

Qy        820 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAG--------GTAATAAACA 871
              ||||||||||||||||||||||||||||||||||||||||||||||||  |     | | |
Db       1267 CCAAATAAGCAAAAGAATGCAGCAAAAAGTAATCTATTACAGTGTTATGCTTTCAGAGCC 1326
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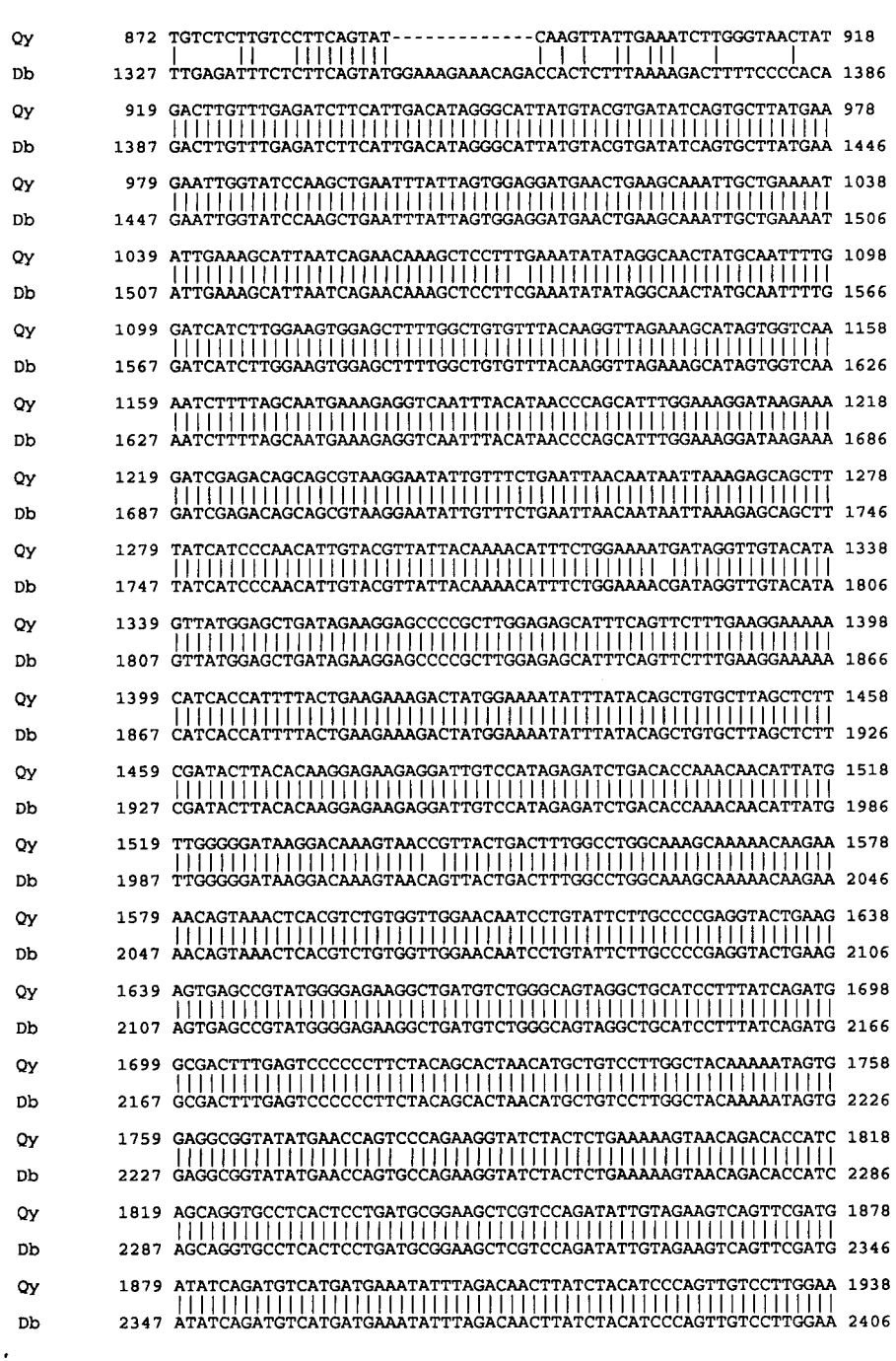
Qy 872 TGTCTCTTGTCCTTCAGTAT----------CAAGTTATTGAAATCTTGGGTAACTAT 918
Db 1327 TTGAGATTTCTCTTCAGTATGGAAAGAAACAGACCACTCTTTAAAAGACTTTTCCCCACA 1386
Qy 919 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 978
Db 1387 GACTTGTTTGAGATCTTCATTGACATAGGGCATTATGTACGTGATATCAGTGCTTATGAA 1446
Qy 979 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1038
Db 1447 GAATTGGTATCCAAGCTGAATTTATTAGTGGAGGATGAACTGAAGCAAATTGCTGAAAAT 1506
Qy 1039 ATTGAAAGCATTAATCAGAACAAAGCTCCTTTGAAATATATAGGCAACTATGCAATTTTG 1098
Db 1507 ATTGAAAGCATTAATCAGAACAAAGCTCCTTCGAAATATATAGGCAACTATGCAATTTTG 1566
Qy 1099 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1158
Db 1567 GATCATCTTGGAAGTGGAGCTTTTGGCTGTGTTTACAAGGTTAGAAAGCATAGTGGTCAA 1626
Qy 1159 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1218
Db 1627 AATCTTTTAGCAATGAAAGAGGTCAATTTACATAACCCAGCATTTGGAAAGGATAAGAAA 1686
Qy 1219 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1278
Db 1687 GATCGAGACAGCAGCGTAAGGAATATTGTTTCTGAATTAACAATAATTAAAGAGCAGCTT 1746
Qy 1279 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAATGATAGGTTGTACATA 1338
Db 1747 TATCATCCCAACATTGTACGTTATTACAAAACATTTCTGGAAAACGATAGGTTGTACATA 1806
Qy 1339 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1398
Db 1807 GTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAGAGCATTTCAGTTCTTTGAAGGAAAAA 1866
Qy 1399 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1458
Db 1867 CATCACCATTTTACTGAAGAAAGACTATGGAAAATATTTATACAGCTGTGCTTAGCTCTT 1926
Qy 1459 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1518
Db 1927 CGATACTTACACAAGGAGAAGAGGATTGTCCATAGAGATCTGACACCAAACAACATTATG 1986
Qy 1519 TTGGGGGATAAGGACAAAGTAACCGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 1578
Db 1987 TTGGGGGATAAGGACAAAGTAACAGTTACTGACTTTGGCCTGGCAAAGCAAAAACAAGAA 2046
Qy 1579 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 1638
Db 2047 AACAGTAAACTCACGTCTGTGGTTGGAACAATCCTGTATTCTTGCCCCGAGGTACTGAAG 2106
Qy 1639 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 1698
Db 2107 AGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTGCATCCTTTATCAGATG 2166
Qy 1699 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 1758
Db 2167 GCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTTGGCTACAAAAATAGTG 2226
Qy 1759 GAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 1818
Db 2227 GAGGCGGTATATGAACCAGTGCCAGAAGGTATCTACTCTGAAAAAGTAACAGACACCATC 2286
Qy 1819 AGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATG 1878
Db 2287 AGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGTAGAAGTCAGTTCGATG 2346
Qy 1879 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 1938
Db 2347 ATATCAGATGTCATGATGAAATATTTAGACAACTTATCTACATCCCAGTTGTCCTTGGAA 2406
Qy 1939 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 1998
Db 2407 AAGAAGCTAGAACGGGAACGAAGACGCACACAAAGGTATTTTATGGAAGCCAACCGGAAC 2466
Qy 1999 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2058
Db 2467 ACCGTCACATGTCACCATGAGCTGGCTGTTCTATCTCACGAGACCTTTGAGAAGGCAAGT 2526
Qy 2059 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2118
Db 2527 TTGAGTAGCAGCAGCAGTGGAGCAGCCAGCCTGAAAAGTGAACTTTCAGAAAGCGCAGAC 2586
Qy 2119 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2178
Db 2587 CTGCCCCCTGAAGGCTTCCAGGCCTCCTATGGTAAAGACGAAGACAGGGCCTGTGACGAA 2646
Qy 2179 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2238
Db 2647 ATCCTGTCAGATGATAACTTCAACCTGGAAAATGCTGAGAAAGATACATATTCAGAGGTA 2706
Qy 2239 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2298
Db 2707 GATGATGAATTGGACATTTCGGATAACTCCAGCAGCTCCAGTTCAAGCCCTCTGAAAGAA 2766
Qy 2299 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 2358
Db 2767 TCTACATTCAACATTTTAAAGAGAAGTTTTAGTGCTTCAGGAGGAGAAAGACAATCCCAA 2826
Qy 2359 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACCAGCTTTGCTGCCTCTTGAC 2418
Db 2827 ACAAGGGACTTCACTGGAGGAACAGGATCAAGACCAAGACC---------- 2867
Qy 2419 CTGCTTCTGAAAGTGCCACCCCACATGCTCAGGGCCCACATTAAGGAAATAGAGGCTGAG 2478
Db 2868 ---------- 2867
Qy 2479 TTAGTGACAGGGTGGCAGTCCCATAGCCTTCCTGCTGTGATTCTTCGAAATCTCAAAGAT 2538
Db 2868 ---------- 2867
Qy 2539 CATGGGCCACAGATGGGCACATTCTTGTGGCAAGCATCAGCAGGAATTGCTGTGTCCCAG 2598
Db 2868 ----------AGCATCAGCAGGAATTGCTGTGTCCCAG 2895
Qy 2599 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2658
Db 2896 AGGAAAGTGCGTCAGATCAGTGATCCTATTCAGCAGATATTAATTCAGCTGCACAAAATA 2955
Qy 2659 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 2718
Db 2956 ATCTATATCACACAGCTTCCTCCAGCTTTGCACCACAATTTGAAAAGAAGGGTTATAGAG 3015
Qy 2719 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 2778
Db 3016 AGATTCAAGAAATCCCTCTTCAGCCAGCAGAGTAACCCTTGTAATTTGAAATCTGAAATT 3075
Qy 2779 AAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTAC 2838
Db 3076 AAAAAGTTATCTCAGGGATCTCCAGAACCGATTGAGCCCAACTTTTTCACAGCAGATTAC 3135
Qy 2839 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 2898
Db 3136 CATTTATTACATCGTTCATCCGGTGGAAACAGCCTGTCCCCAAATGACCCTACAGGTTTA 3195
Qy 2899 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 2958
Db 3196 CCAACCAGCATTGAATTGGAGGAAGGAATAACATATGAACAGATGCAGACTGTGATTGAA 3255
Qy 2959 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3018
Db 3256 GAAGTCCTTGAGGAAAGTGGCTATTACAATTTTACATCTAACAGGTATCATTCCTATCCA 3315
Qy 3019 TGGGGGACCAAGAATCACCCAACCAAAAGATGA 3051

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Db       3316 TGGGGGACCAAGAATCACCCAACCAAAAGATGA 3348


RESULT 3
US-09-621-976-2174
; Sequence 2174, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2174
;   LENGTH: 564
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 262..525
US-09-621-976-2174

  Query Match             6.9%;  Score 252;  DB 4;  Length 564;
  Best Local Similarity   99.3%;  Pred. No. 5.4e-64;
  Matches  274;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy       1623 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 1682
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Db        288 CCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCTGGGCAGTAGGCTG 347

Qy       1683 CATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCTACAGCACTAACATGCTGTCCTT 1742
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Qy       1743 GGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAGAAGGTATCTACTCTGAAAA 1802
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Qy       1803 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAAGCTCGTCCAGATATTGT 1862
             ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        468 AGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGGAA-CTCGTCCAGATATTGT 526

Qy       1863 AGAAGTCAGTTCGATGATATCAGATGTCATGATGAA 1898
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Db        527 AGAAGTCAG-TCGATGATATCAGATGTCATGATGAA 561


RESULT 4
US-09-221-235-3
; Sequence 3, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,235
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(906)
US-09-221-235-3

  Query Match             2.2%;  Score 79;  DB 3;  Length 906;
  Best Local Similarity   49.1%;  Pred. No. 1.8e-12;
  Matches  301;  Conservative    0;  Mismatches  300;  Indels   12;  Gaps    3;

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Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
              |  | ||| || ||    |  |||||||| |||| ||   ||| |  | |   ||
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
                 |||    ||| ||| |  || |    |  || |||||  ||   | |||||
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
                |||  | ||||| |||    ||  |   | || | |  |          ||  |  | ||||
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
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Db        479 GAGATATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTGGAGATC 538

Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
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Db        539 TTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCACATTCTTTAGTTGGTACGC 598

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Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
              || |  | |||||  | || ||| |||||||  | ||      || ||||      |||
Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
                |  ||  |    ||  ||  ||  || ||||   ||   |  ||   |||  | ||
Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
              || |  ||| || ||| || |  | |     | |  | |||| |||  || ||| | |
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
              |    || |||||
Db        839 AGAAGCGACCAGA 851


RESULT 5
US-09-221-928-3
; Sequence 3, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,928
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(906)
US-09-221-928-3
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  Query Match             2.2%;  Score 79;  DB 3;  Length 906;
  Best Local Similarity   49.1%;  Pred. No. 1.8e-12;
  Matches  301;  Conservative    0;  Mismatches  300;  Indels   12;  Gaps    3;

Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
              ||  || |    ||     |||| ||  | ||||| ||  |  ||   |||||   | |||
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
              |  | ||| || ||    | |||||||| |||| ||   ||| |  | |   ||
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
                |||    ||| ||| |  || |    || |||||  ||   | |||||
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
               ||| | ||||| |||   ||  |   | || | |   |        ||  |  | ||||
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
              |||||  | | ||||   ||  |  |  |     |||   ||   ||
Db        479 GAGATATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTGGAGATC 538

Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
              ||||  || |    |                ||| |  | |    |   ||| | ||||| ||
Db        539 TTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCACATTCTTTAGTTGGTACGC 598

Qy       1610 TCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCT 1669
                 ||   |  || ||| | | |    |   ||       ||  |||| |||
Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
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Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
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Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
                || |  ||| || ||| || |   | |     | |  | |||| |||  || ||| | |
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
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Db        839 AGAAGCGACCAGA 851
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RESULT 6
US-09-221-527-3
; Sequence 3, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,527
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(906)
US-09-221-527-3
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  Query Match             2.2%;  Score 79;  DB 3;  Length 906;
  Best Local Similarity   49.1%;  Pred. No. 1.8e-12;
  Matches  301;  Conservative    0;  Mismatches  300;  Indels   12;  Gaps    3;

Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
              ||  || |    ||     |||| ||  | ||||| ||  |  ||   |||||   | |||
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
              |  | ||| || ||    | |||||||| |||| ||   ||| |  | |   ||
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
                |||    ||| ||| |  || |    || |||||  ||   | |||||
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
               ||| | ||||| |||   ||  |   | || | |   |        ||  |  | ||||
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
              |||||  | | ||||   ||  |  |  |     |||   ||   ||
Db        479 GAGATATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTGGAGATC 538

Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
              ||||  || |    |                ||| |  | |    |   ||| | ||||| ||
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Qy       1610 TCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCT 1669
                 ||   |  || ||| | | |    |   ||       ||  |||| |||
Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
              ||  |  | |||||  | || ||| |||||||  | ||       || ||||      |||
Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
                |  ||  |    ||  ||  ||  || ||||   ||   |  ||   ||| | ||
Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
                || |  ||| || ||| || |   | |     | |  | |||| |||  || ||| | |
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
                |   || |||||
Db        839 AGAAGCGACCAGA 851
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RESULT 7
US-09-221-236-3
; Sequence 3, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,236
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(906)
US-09-221-236-3
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  Query Match             2.2%;  Score 79;  DB 3;  Length 906;
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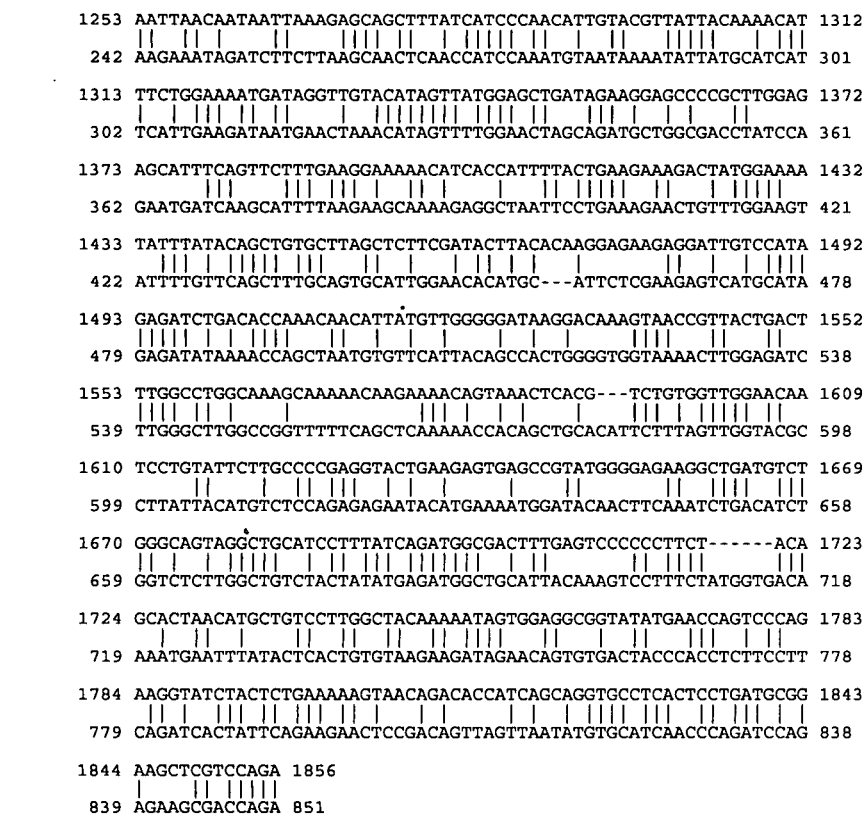
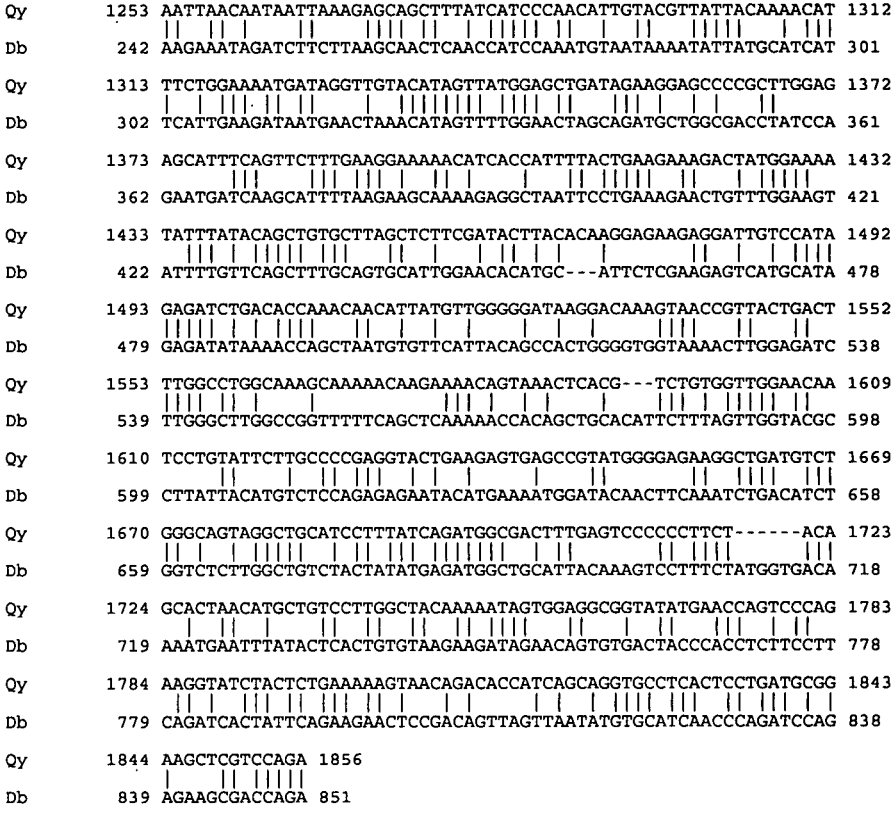
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;



RESULT 8
US-09-221-416-3
; Sequence 3, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(906)
US-09-221-416-3

Query Match 2.2%; Score 79; DB 3; Length 906;
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;



RESULT 9
US-09-221-245-3
; Sequence 3, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: US 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(906)
US-09-221-245-3

Query Match 2.2%; Score 79; DB 3; Length 906;
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;

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Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
Db        479 GAGATATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTGGAGATC 538

Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
Db        539 TTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCACATTCTTTAGTTGGTACGC 598

Qy       1610 TCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCT 1669
Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
Db        839 AGAAGCGACCAGA 851
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RESULT 10
US-09-163-115-3
; Sequence 3, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(906)
US-09-163-115-3

Query Match 2.2%; Score 79; DB 3; Length 906;
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;

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Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
Db        479 GAGATATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTGGAGATC 538

Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
Db        539 TTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCACATTCTTTAGTTGGTACGC 598

Qy       1610 TCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCT 1669
Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
Db        839 AGAAGCGACCAGA 851
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RESULT 11
US-09-221-528-3
; Sequence 3, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(906)
US-09-221-528-3

Query Match 2.2%; Score 79; DB 3; Length 906;
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;

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Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301
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Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
Db        479 GAGATATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTGGAGATC 538

Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
Db        539 TTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCACATTCTTTAGTTGGTACGC 598

Qy       1610 TCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCT 1669
Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
Db        839 AGAAGCGACCAGA 851
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RESULT 12
US-09-593-553-3
; Sequence 3, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/593,553
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(906)
US-09-593-553-3

Query Match 2.2%; Score 79; DB 3; Length 906;
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;

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Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
Db        302 TCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA 361

Qy       1373 AGCATTTCAGTTCTTTGAAGGAAAAACATCACCATTTTACTGAAGAAAGACTATGGAAAA 1432
Db        362 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGT 421

Qy       1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
Db        422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478

Qy       1493 GAGATCTGACACCAAACAACATTATGTTGGGGGATAAGGACAAAGTAACCGTTACTGACT 1552
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Qy       1553 TTGGCCTGGCAAAGCAAAAACAAGAAAACAGTAAACTCACG---TCTGTGGTTGGAACAA 1609
Db        539 TTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCACATTCTTTAGTTGGTACGC 598

Qy       1610 TCCTGTATTCTTGCCCCGAGGTACTGAAGAGTGAGCCGTATGGGGAGAAGGCTGATGTCT 1669
Db        599 CTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAATCTGACATCT 658

Qy       1670 GGGCAGTAGGCTGCATCCTTTATCAGATGGCGACTTTGAGTCCCCCCTTCT------ACA 1723
Db        659 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACA 718

Qy       1724 GCACTAACATGCTGTCCTTGGCTACAAAAATAGTGGAGGCGGTATATGAACCAGTCCCAG 1783
Db        719 AAATGAATTTATACTCACTGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTT 778

Qy       1784 AAGGTATCTACTCTGAAAAAGTAACAGACACCATCAGCAGGTGCCTCACTCCTGATGCGG 1843
Db        779 CAGATCACTATTCAGAAGAACTCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAG 838

Qy       1844 AAGCTCGTCCAGA 1856
Db        839 AGAAGCGACCAGA 851
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RESULT 13
US-09-221-237-3
; Sequence 3, Application US/09221237
; Patent No. 6214597
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,237
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(906)
US-09-221-237-3

Query Match 2.2%; Score 79; DB 3; Length 906;
Best Local Similarity 49.1%; Pred. No. 1.8e-12;
Matches 301; Conservative 0; Mismatches 300; Indels 12; Gaps 3;

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Qy       1253 AATTAACAATAATTAAAGAGCAGCTTTATCATCCCAACATTGTACGTTATTACAAAACAT 1312
Db        242 AAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAATATTATGCATCAT 301

Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
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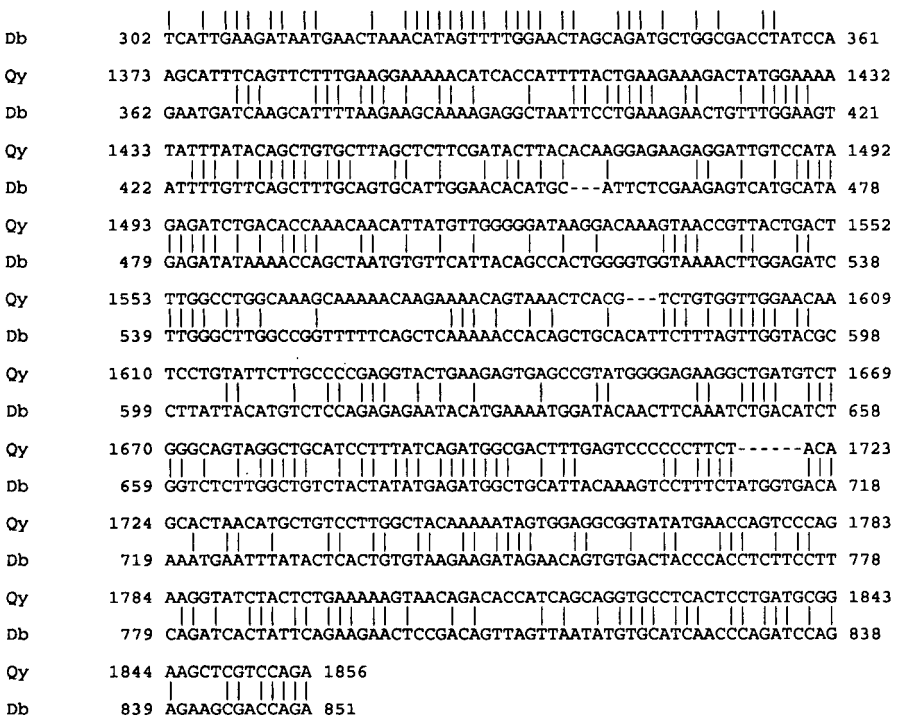
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Qy 1433 TATTTATACAGCTGTGCTTAGCTCTTCGATACTTACACAAGGAGAAGAGGATTGTCCATA 1492
Db 422 ATTTTGTTCAGCTTTGCAGTGCATTGGAACACATGC---ATTCTCGAAGAGTCATGCATA 478
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; Sequence 3, Application US/09757982
; Patent No. 6740737
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/757,982
;  CURRENT FILING DATE:  2001-01-10
;  PRIOR APPLICATION NUMBER: 09/163,115
;  PRIOR FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(906)
US-09-757-982-3

  Query Match             2.2%;  Score 79;  DB 4;  Length 906;
  Best Local Similarity   49.1%;  Pred. No. 1.8e-12;
  Matches  301;  Conservative    0;  Mismatches  300;  Indels   12;  Gaps    3;

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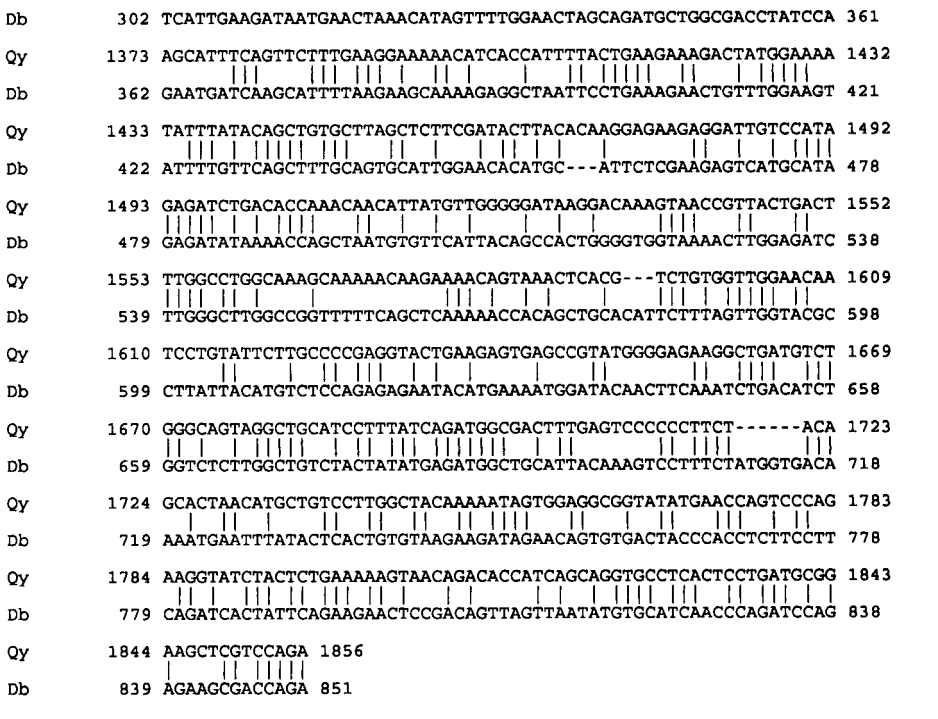
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Qy 1844 AAGCTCGTCCAGA 1856
Db 839 AGAAGCGACCAGA 851

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; Sequence 1, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,235
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4137
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: 'n' at positions 2872, 3597 and 3682 may be any nucleic acid
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (297)..(1202)
US-09-221-235-1

  Query Match             2.2%;  Score 79;  DB 3;  Length 4137;
  Best Local Similarity   49.1%;  Pred. No. 5.2e-12;
  Matches  301;  Conservative    0;  Mismatches  300;  Indels   12;  Gaps    3;

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Qy       1313 TTCTGGAAAATGATAGGTTGTACATAGTTATGGAGCTGATAGAAGGAGCCCCGCTTGGAG 1372
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OM protein - protein search, using sw model

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SUMMARIES

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2	4149	79.6	854	4	US-10-335-711-9	Sequence 9, Appli
3	441	8.5	451	4	US-09-248-796A-18414	Sequence 18414, A
4	440	8.4	306	4	US-09-949-016-6871	Sequence 6871, Ap
5	440	8.4	356	4	US-09-949-016-9705	Sequence 9705, Ap
6	438	8.4	302	3	US-09-221-235-2	Sequence 2, Appli
7	438	8.4	302	3	US-09-221-928-2	Sequence 2, Appli
8	438	8.4	302	3	US-09-221-527-2	Sequence 2, Appli
9	438	8.4	302	3	US-09-221-236-2	Sequence 2, Appli
10	438	8.4	302	3	US-09-221-416-2	Sequence 2, Appli
11	438	8.4	302	3	US-09-221-245-2	Sequence 2, Appli
12	438	8.4	302	3	US-09-163-115-2	Sequence 2, Appli
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15	438	8.4	302	3	US-09-221-237-2	Sequence 2, Appli
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43	393.5	7.5	293	3	US-09-295-068-1	Sequence 1, Appli
44	393.5	7.5	293	4	US-09-481-275-1	Sequence 1, Appli
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ALIGNMENTS

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US-10-335-711-2
; Sequence 2, Application US/10335711
; Patent No. 6759222
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 14815, A Human Kinase Family Member and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: MPI02-002P1RNM
; CURRENT APPLICATION NUMBER: US/10/335,711
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/345,853
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-711-2

Query Match 86.6%; Score 4516.5; DB 4; Length 1115;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 906; Conservative 8; Mismatches 26; Indels 113; Gaps 5;

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Qy         271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
               |||||||||||||||||          |:     : : |   ||||||||||||||||
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Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
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Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
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Qy        684 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 743
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RESULT 2
US-10-335-711-9
; Sequence 9, Application US/10335711
; Patent No. 6759222
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 14815, A Human Kinase Family Member and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: MPI02-002P1RNM
; CURRENT APPLICATION NUMBER: US/10/335,711
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/345,853
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-711-9

Query Match 79.6%; Score 4149; DB 4; Length 854;
Best Local Similarity 91.8%; Pred. No. 1.3e-313;

Matches 827; Conservative 4; Mismatches 16; Indels 54; Gaps 2;

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Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP---------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
Db        808 -------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
Db        854 P 854
```

RESULT 3
US-09-248-796A-18414
; Sequence 18414, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18414
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18414

Query Match 8.5%; Score 441; DB 4; Length 451;
Best Local Similarity 27.9%; Pred. No. 7.7e-26;
Matches 143; Conservative 66; Mismatches 169; Indels 134; Gaps 18;

Qy 357 LKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRN-I 415
Db 24 MSIIDEYESLEVIGKGSFGTVRRVRHKDGQ-ILVRKEI---------EYTSMTSQERNHI 73

Qy 416 VSELTIIKEQLYHPNIVRYYK--TFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
Db 74 ISELRILRE-LDHPHIVKYYRHDHIPEKKMIHIYMEYCEGGDLAKVIKNFRASKSRIPEE 132

Qy 474 RLWKIFIQLCLALRYLH----KEK-------------RIVHRDLTPNNIMLGDKDKVTV 515
Db 133 FVWQVLVQVLLALYRCHYGVDAEKVNLFKTALEPKYANSIIHRDIKPDNIFVG--SCIKL 190

Qy 516 TDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYS 575
Db 191 GDFGLAKMLSANDFAKTYVGTPYYMSPEVLLDDPYSPVCDIWSLGCVLYELCTLEPPFKA 250

Qy 576 TNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYL 635
Db 251 KSHLQLQAKIKRGVIEEVPD-FYSLQLRTLIRLCITVDPEERPTCFDL----------I 298

Qy 636 DNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAA 695
Db 299 DSLAVRFLRKEMELK----------EMNENL----------EEYKKQLLKRS----- 330

Qy 696 SLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNL-----ENAEKDTYSEVDDEL 750
Db 331 ---KELKETSKELDEYKQELVRKSEELSKREKYLDEEFELRKQAIELESKEIRMEYQREF 387

Qy 751 DI----------SDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTG 792
Db 388 NLVVEQEVKRRLEQRKPHGPRPLEDVSPRSPLKER---------- 422

Qy 793 GTGSRPRPALLPLDLLLKVPPHMLRAHIKEIE 824
Db 423 ---NRPRVT----DALERL--HLEKRHTPEFE 445

RESULT 4
US-09-949-016-6871
; Sequence 6871, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6871
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6871

Query Match 8.4%; Score 440; DB 4; Length 306;
Best Local Similarity 34.8%; Pred. No. 5.1e-26;
Matches 92; Conservative 54; Mismatches 106; Indels 12; Gaps 5;

Qy 360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
Db 35 LADFQIEKKIGRGQFSEVYKATCLLDRKTVALKKVQIFEMMDAKARQD-------CVKEI 87

Qy 420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
Db 88 GLLK-QLNHPNIIKYLDSFIEDNELNIVLELADAGDLSQMIKYFKKQKRLIPERTVWKYF 146

Qy 480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK-QKQENSKLTSVVGTIL 538
Db 147 VQLCSAVEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLGRFFSSETTAAHSLVGTPY 205

Qy 539 YSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVPEG 596
Db 206 YMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLFSLCQKIEQCDYPPLPGE 265

Qy 597 IYSEKVTDTISRCLTPDAEARPDI 620
Db 266 HYSEKLRELVSMCICPDPHQRPDI 289

RESULT 5
US-09-949-016-9705
; Sequence 9705, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9705
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9705

Query Match 8.4%; Score 440; DB 4; Length 356;
Best Local Similarity 34.8%; Pred. No. 6.4e-26;
Matches 92; Conservative 54; Mismatches 106; Indels 12; Gaps 5;

Qy 360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
Db 85 LADFQIEKKIGRGQFSEVYKATCLLDRKTVALKKVQIFEMMDAKARQD-------CVKEI 137

Qy 420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
Db 138 GLLK-QLNHPNIIKYLDSFIEDNELNIVLELADAGDLSQMIKYFKKQKRLIPERTVWKYF 196

Qy 480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK-QKQENSKLTSVVGTIL 538

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Db        197 VQLCSAVEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLGRFFSSETTAAHSLVGTPY 255

Qy        539 YSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVPEG 596

Db        256 YMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLFSLCQKIEQCDYPPLPGE 315

Qy        597 IYSEKVTDTISRCLTPDAEARPDI 620

Db        316 HYSEKLRELVSMCICPDPHQRPDI 339


RESULT 6
US-09-221-235-2
; Sequence 2, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,235
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-235-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419

Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479

Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536

Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594

Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623

Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


RESULT 7
US-09-221-928-2
; Sequence 2, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,928
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-928-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419

Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479

Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536

Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594

Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623

Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


RESULT 8
US-09-221-527-2
; Sequence 2, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,527
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-527-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419

Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479

Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536

Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594

Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623

Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288
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RESULT 9
US-09-221-236-2
; Sequence 2, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,236
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-236-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : |: |   :| | |  ||:         :|:|:| : :    | : |        : |:
Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| || |||:::|| :|:|:: | ||:|| :   |       |::     |  :|| |
Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
              :||| || ::|  :|::|||: | |: :     | : | ||   :  :|| |   |:|||
Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594
                | || :    |  |:|:|::||:||:|| |  |||    |: ||  || :  | |:|
Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623
                |||::   :: |: || | |||:  |
Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


RESULT 10
US-09-221-416-2
; Sequence 2, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,416
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-416-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : |: |   :| | |  ||:         :|:|:| : :    | : |        : |:
Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| || |||:::|| :|:|:: | ||:|| :   |       |::     |  :|| |
Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
              :||| || ::|  :|::|||: | |: :     | : | ||   :  :|| |   |:|||
Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594
                | || :    |  |:|:|::||:||:|| |  |||    |: ||  || :  | |:|
Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623
                |||::   :: |: || | |||:  |
Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


RESULT 11
US-09-221-245-2
; Sequence 2, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,245
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: US 09/163,115
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-245-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : |: |   :| | |  ||:         :|:|:| : :    | : |        : |:
Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| || |||:::|| :|:|:: | ||:|| :   |       |::     |  :|| |
Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
              :||| || ::|  :|::|||: | |: :     | : | ||   :  :|| |   |:|||
Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594
                | || :    |  |:|:|::||:||:|| |  |||    |: ||  || :  | |:|
Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623
                |||::   :: |: || | |||:  |
Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


RESULT 12
US-09-163-115-2
; Sequence 2, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/163,115A
;  CURRENT FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-163-115-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : |: |   :| | |  ||:         :|:|:| : :    | : |        : |:
Db         31 LANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIFDLMDAKARAD-------CIKEI 83

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
             ::| || |||:::|| :|:|:: | ||:|| :   |       |::     |  :|| |
Db         84 DLLK-QLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYF 142

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Db        200 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 259

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623
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Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


RESULT 13
US-09-221-528-2
; Sequence 2, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,528
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-528-2

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  Best Local Similarity   34.6%;  Pred. No. 7.1e-26;
  Matches   93;  Conservative   55;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
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Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
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Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623
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RESULT 14
US-09-593-553-2
; Sequence 2, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan
;  TITLE OF INVENTION:  NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE:  MNI-050
;  CURRENT APPLICATION NUMBER: US/09/593,553
;  CURRENT FILING DATE:  2000-06-14
;  PRIOR APPLICATION NUMBER:  09/163,115
;  PRIOR FILING DATE:  1998-09-28
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-593-553-2

  Query Match             8.4%;  Score 438;  DB 3;  Length 302;
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Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
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RESULT 15
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; Sequence 2, Application US/09221237
; Patent No. 6214597
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan
;  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-050
;  CURRENT APPLICATION NUMBER: US/09/221,237
;  CURRENT FILING DATE: 1998-12-28
;  EARLIER APPLICATION NUMBER: 09/163,115
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 15
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;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-221-237-2

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Db        143 VQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 199

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594
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Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV 623
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Db        260 SDHYSEELRQLVNMCINPDPEKRPDVTYV 288


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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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2244.612 Million cell updates/sec

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Perfect score: 5214
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Maximum Match 100%
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SUMMARIES

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1	5214	100.0	1016	15	US-10-684-190-2	Sequence 2, Appli
2	4587.5	88.0	1125	16	US-10-618-941-93	Sequence 93, Appl
3	4516.5	86.6	1115	14	US-10-335-711-2	Sequence 2, Appli
4	4149	79.6	854	14	US-10-335-711-9	Sequence 9, Appli
5	4149	79.6	854	15	US-10-220-955-14	Sequence 14, Appl
6	4149	79.6	854	15	US-10-684-190-4	Sequence 4, Appli
7	2451	47.0	484	15	US-10-094-749-3007	Sequence 3007, Ap
8	2110.5	40.5	488	15	US-10-425-114-37531	Sequence 37531, A
9	1172	22.5	229	9	US-09-764-868-847	Sequence 847, App
10	1156	22.2	1895	16	US-10-399-136-3	Sequence 3, Appli
11	1129	21.7	223	11	US-09-764-875-687	Sequence 687, App
12	980.5	18.8	261	16	US-10-399-136-2	Sequence 2, Appli
13	520	10.0	106	9	US-09-764-868-1168	Sequence 1168, Ap
14	520	10.0	106	10	US-09-764-891-4539	Sequence 4539, Ap
15	520	10.0	106	11	US-09-764-875-1003	Sequence 1003, Ap
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21	440	8.4	361	15	US-10-425-114-37522	Sequence 37522, A
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27	435	8.3	302	14	US-10-355-975-9	Sequence 9, Appli
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29	423	8.1	445	14	US-10-354-358-58	Sequence 58, Appl
30	423	8.1	445	15	US-10-173-999-30	Sequence 30, Appl
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32	423	8.1	445	15	US-10-058-270A-96	Sequence 96, Appl
33	423	8.1	445	15	US-10-188-832-157	Sequence 157, App
34	412	7.9	384	15	US-10-351-738A-24	Sequence 24, Appl
35	411.5	7.9	256	10	US-09-823-187-96	Sequence 96, Appl
36	411	7.9	654	9	US-09-940-921B-4	Sequence 4, Appli
37	410.5	7.9	889	16	US-10-618-941-94	Sequence 94, Appl
38	408.5	7.8	249	9	US-09-764-868-812	Sequence 812, App
39	407	7.8	425	15	US-10-114-270-184	Sequence 184, App
40	406.5	7.8	251	15	US-10-042-865-101	Sequence 101, App
41	406.5	7.8	252	10	US-09-976-782-41	Sequence 41, Appl
42	406.5	7.8	254	10	US-09-976-782-30	Sequence 30, Appl
43	406.5	7.8	254	15	US-10-074-978A-151	Sequence 151, App
44	406.5	7.8	256	10	US-09-863-776-41	Sequence 41, Appl
45	406.5	7.8	256	11	US-09-964-956-74	Sequence 74, Appl

ALIGNMENTS

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US-10-684-190-2
; Sequence 2, Application US/10684190
; Publication No. US20040096889A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMA
; TITLE OF INVENTION: KINASE
; FILE REFERENCE: AM101073
; CURRENT APPLICATION NUMBER: US/10/684,190
; CURRENT FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1016
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-190-2

Query Match 100.0%; Score 5214; DB 15; Length 1016;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        301 EILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYI 360
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Qy        781 GERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVI 840
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; Sequence 93, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
;  APPLICANT: WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  CAENEPEEL, SEAN
;  TITLE OF INVENTION: NOVEL KINASES
;  FILE REFERENCE: 034536-0321
;  CURRENT APPLICATION NUMBER: US/10/618,941
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: 60/395,632
;  PRIOR FILING DATE: 2002-07-15
;  NUMBER OF SEQ ID NOS: 143
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
;   LENGTH: 1125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-618-941-93

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                                         ||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              |||||||||||||||||          |:     : : |   ||||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 719

Qy        564 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 779

Qy        624 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 839

Qy        684 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 899

Qy        744 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALL 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRP--- 956

Qy        804 PLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIA 863
                                                 ||||||||||||||||
Db        957 ------------------------------------------GPQMGTFLWQASAGIA 972

Qy        864 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 1032
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```
Qy        924 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 1092

Qy        984 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              |||||||||||||||||||||||||||||||||
Db       1093 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1125


RESULT 3
US-10-335-711-2
; Sequence 2, Application US/10335711
; Publication No. US20030134317A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel E.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 14815, A Human Kinase Family Member and
;  TITLE OF INVENTION:  Uses Therefor
;  FILE REFERENCE: MPI02-002P1RNM
;  CURRENT APPLICATION NUMBER: US/10/335,711
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: 60/345,853
;  PRIOR FILING DATE: 2002-01-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1115
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-335-711-2

  Query Match             86.6%;  Score 4516.5;  DB 14;  Length 1115;
  Best Local Similarity   86.0%;  Pred. No. 1.6e-279;
  Matches  906;  Conservative    8;  Mismatches   26;  Indels  113;  Gaps    5;

Qy         12 PTVYFKN------------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQ 59
              |:::|              |    | |||         : :  ||||||||||||||||||
Db        128 PSIHFLRVLICLRLLMRDPCYQEILHSLGG--------IENLAQYMEIVANEYLGYGEEQ 179

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAES 239

Qy        119 ----------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                         ||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              |||||||||||||||||          |:     : : |   ||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 719

Qy        564 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 779

Qy        624 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 839

Qy        684 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 899

Qy        744 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALL 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRP--- 956

Qy        804 PLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIA 863
                                                                ||||||
Db        957 ------------------------------------------------------ASAGIA 962

Qy        864 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 1022

Qy        924 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 1082

Qy        984 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              |||||||||||||||||||||||||||||||||
Db       1083 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1115


RESULT 4
US-10-335-711-9
; Sequence 9, Application US/10335711
; Publication No. US20030134317A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel E.
;  APPLICANT:  Millennium Pharmaceuticals, Inc.
;  TITLE OF INVENTION: 14815, A Human Kinase Family Member and
;  TITLE OF INVENTION:  Uses Therefor
;  FILE REFERENCE: MPI02-002P1RNM
;  CURRENT APPLICATION NUMBER: US/10/335,711
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: 60/345,853
;  PRIOR FILING DATE: 2002-01-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 854
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-335-711-9

  Query Match             79.6%;  Score 4149;  DB 14;  Length 854;
  Best Local Similarity   91.8%;  Pred. No. 3.4e-256;
  Matches  827;  Conservative    4;  Mismatches   16;  Indels   54;  Gaps    2;

Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLCAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60

Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
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Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQV-------INMSL 293
              ||||||||||||||||||||||||||||||||||||||||||||||||          |:
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQCYAFRALRFLFSM 300

Qy        294 VLQYQVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 353
                  : : |   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ERNRPLFKRLFPTDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 360

Qy        354 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 420

Qy        414 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 480

Qy        474 RLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 533
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 RLWKIFIQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 540

Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
              ||||||||||||||||||||||||||
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP---------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
                              ||||||||||||||||||||||||||||||||||||||||||||
Db        808 --------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
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Db        854 P 854
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RESULT 5
US-10-220-955-14
; Sequence 14, Application US/10220955
; Publication No. US20030211989A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602-1401
; CURRENT APPLICATION NUMBER: US/10/220,955
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-955-14

Query Match 79.6%; Score 4149; DB 15; Length 854;
Best Local Similarity 91.8%; Pred. No. 3.4e-256;
Matches 827; Conservative 4; Mismatches 16; Indels 54; Gaps 2;

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Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLCAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60

Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180

Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQV-------INMSL 293
              ||||||||||||||||||||||||||||||||||||||||||||||||          |:
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQCYAFRALRFLFSM 300

Qy        294 VLQYQVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 353
                  : : |   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ERNRPLFKRLFPTDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 360

Qy        354 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 420

Qy        414 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 480

Qy        474 RLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 533
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 RLWKIFIQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 540

Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
              ||||||||||||||||||||||||||
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP---------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
                              ||||||||||||||||||||||||||||||||||||||||||||
Db        808 --------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
              |
Db        854 P 854
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RESULT 6

```
US-10-684-190-4
; Sequence 4, Application US/10684190
; Publication No. US20040096889A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
;  TITLE OF INVENTION:  KINASE
;  FILE REFERENCE: AM101073
;  CURRENT APPLICATION NUMBER: US/10/684,190
;  CURRENT FILING DATE:  2003-10-10
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 854
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-190-4

  Query Match             79.6%;  Score 4149;  DB 15;  Length 854;
  Best Local Similarity   91.8%;  Pred. No. 3.4e-256;
  Matches  827;  Conservative    4;  Mismatches   16;  Indels   54;  Gaps    2;

Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLCAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60

Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180

Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQV-------INMSL 293
              ||||||||||||||||||||||||||||||||||||||||||||||||           |:
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQCYAFRALRFLFSM 300

Qy        294 VLQYQVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 353
                  : :  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ERNRPLFKRLFPTDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 360

Qy        354 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 420

Qy        414 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 480

Qy        474 RLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 533
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 RLWKIFIQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 540

Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
              |||||||||||||||||||||||||||
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP---------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 --------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
              |
Db        854 P 854


RESULT 7
US-10-094-749-3007
; Sequence 3007, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
;  FILE REFERENCE: 084335/0160
;  CURRENT APPLICATION NUMBER: US/10/094,749
;  CURRENT FILING DATE:  2002-03-12
;  PRIOR APPLICATION NUMBER: 60/350,435
;  PRIOR FILING DATE: 2002-01-24
;  PRIOR APPLICATION NUMBER: JP 2001-328381
;  PRIOR FILING DATE: 2001-09-14
;  NUMBER OF SEQ ID NOS: 3381
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3007
;   LENGTH: 484
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-094-749-3007

  Query Match             47.0%;  Score 2451;  DB 15;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-148;
  Matches  475;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        542 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 601
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 69

Qy        602 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 661
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 129

Qy        662 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 721
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 189

Qy        722 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 781
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 249
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Qy        782 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 309

Qy        842 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 369

Qy        902 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 429

Qy        962 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 484


RESULT 8
US-10-425-114-37531
; Sequence 37531, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37531
;   LENGTH: 488
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4119-205-A2_FLI.pep
US-10-425-114-37531

  Query Match             40.5%;  Score 2110.5;  DB 15;  Length 488;
  Best Local Similarity   88.0%;  Pred. No. 2.3e-126;
  Matches  418;  Conservative    0;  Mismatches    0;  Indels   57;  Gaps    1;

Qy        542 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 130

Qy        602 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 190

Qy        662 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 250

Qy        722 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 310

Qy        782 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 841
              ||||||||||||||||||
Db        311 ERQSQTRDFTGGTGSRPRP---------------------------------------- 329

Qy        842 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 901
                                  ||||||||||||||||||||||||||||||||||||||
Db        330 ----------------ASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 373

Qy        902 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 433

Qy        962 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 488


RESULT 9
US-09-764-868-847
; Sequence 847, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ32
;  CURRENT APPLICATION NUMBER: US/09/764,868
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 1510
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 847
;   LENGTH: 229
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (119)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-847

  Query Match             22.5%;  Score 1172;  DB 9;  Length 229;
  Best Local Similarity   99.1%;  Pred. No. 7.1e-67;
  Matches  227;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        312 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGS 371
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGS 60

Qy        372 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNI 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         61 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPXI 120

Qy        432 VRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHK 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHK 180

Qy        492 EKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 229


RESULT 10
US-10-399-136-3
; Sequence 3, Application US/10399136
; Publication No. US20040101529A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer AG
;  TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE
;  FILE REFERENCE: LIO183 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/399,136
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/240.067
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1895
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-10-399-136-3

  Query Match             22.2%;  Score 1156;  DB 16;  Length 1895;
  Best Local Similarity   30.4%;  Pred. No. 1.3e-64;
  Matches  312;  Conservative  184;  Mismatches  296;  Indels  236;  Gaps   31;
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Qy         13 TVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH----TVDKLVNM 68
Db        116 TKSYRNCK--------------------FQTFQFIASRFL---RSEHDWNVTVVNCLNV 151

Qy         69 TYIFQKLA-AVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE--------R 119
Db        152 T---QKLIDNGENARKFVDCNLEDAVLV-LLATRQMTVLQHSLEILGRLSDWSTTCRENL 207

Qy        120 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEI 179
Db        208 LCISLLRILSCEEQAREQIRIYDGVPTLLGLLSIKNSRLQWHVAWTLAQLAEQHETSLEI 267

Qy        180 RIWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQ 239
Db        268 AQLGGISLIF----------------------AA-------ISNPKPPGKAVGDWVAML 297

Qy        240 AACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKS----NLLQV-INMSLV 294
Db        298 TGLTALLAQLAQASSNQQLMSNANGVYILGKLLAIKKNVTTDETIDSWDLLQCSIFRVLR 357

Qy        295 LQY------QVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIE 348
Db        358 LMYTFERSRQLLKKVLPTEIFEKFVDVGNYNSVLTDYDQIAKMYDNLIEENI-EIMKDWE 416

Qy        349 SINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRK----HSGQ--NLLAMKEVNLHNPAFG 402
Db        417 TVNERRQAVGEVGEYELLDQLGAGAFGCVYTVRKKAQSHSENPAKLLALKEIFMTN---- 472

Qy        403 KDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSS 462
Db        473 LNDRESDKSFGDMISEVKIIKQQLRHPNIVRYRRIFVENHRLYIVMDLIQGCSLRDLIIT 532

Qy        463 LKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK 522
Db        533 MKEKKGNFEEKKIWAMVVQMMLALRYLHKEKQIVHRDLKPNNIMMTTDERVVITDFGLAK 592

Qy        523 QKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLA 582
Db        593 QKGP-EYLKSAAGTIIYSCPEIVQNLPYGEKADIWSFGCCIYEMCQLQPVFHSTNMLTLA 651

Qy        583 TKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQ 642
Db        652 MQIVEAKYDPLNE-MWSDDLRFLITSCLAPDPSARPDILKVSGMCGVRLLEYLDDVARQQ 710

Qy        643 LSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELS 702
Db        711 ---------------------------------------------ASTSDMTAS------ 719

Qy        703 ESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSS 762
Db        720 ----------QSSY----------------------------NIKIDESPSSLNSSTS 739

Qy        763 PLKESTFNILKRSFSASGGER-----QSQTRDFTGGTGSRPRPA---LLP-----LDLLL 809
Db        740 SYKRP-----GRSSKTSGSGKLPPINPAPRRNHSMSAGETPRPSSIVCLPRITDKYSVMF 794

Qy        810 KVPPHML--RAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQR 867
Db        795 PSAPSAIPSRRRVQTCSTE-------HPARSSSSTELK---------VSKQSDGLTVSSN 838

Qy        868 KVRQISDPIQQILILQLHKIIYITQ---LPPALHHNLKRRVIERFKKSLFSQQSNPCNLKS 924
Db        839 VLRQIQDPVLTILNQIHRILVVTDKETISTSMNH--QRRLVEMFRKNLLGRENDAVQMKT 896

Qy        925 EIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQTV 984
Db        897 HLRKLAAESPEEIQMNLGFSDFRPVLVQSHINGYQKDQKV---------TKITYEQLSAC 947

Qy        985 IEEVLEES 992
Db        948 IECLIAEN 955
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RESULT 11
US-09-764-875-687
; Sequence 687, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ02
;  CURRENT APPLICATION NUMBER: US/09/764,875
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 1249
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 687
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-764-875-687

  Query Match             21.7%;  Score 1129;  DB 11;  Length 223;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-64;
  Matches  219;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        321 DISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKV 380
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          4 DISAYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKV 63

Qy        381 RKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLE 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 RKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLE 123

Qy        441 NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDL 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDL 183

Qy        501 TPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
              |||||||||||||||||||||||||||||||||||||||
Db        184 TPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 223


RESULT 12
US-10-399-136-2
; Sequence 2, Application US/10399136
; Publication No. US20040101529A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer AG
;  TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE
;  FILE REFERENCE: LIO183 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/399,136
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/240.067
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-399-136-2

  Query Match             18.8%;  Score 980.5;  DB 16;  Length 261;
  Best Local Similarity   45.0%;  Pred. No. 1.4e-54;
  Matches  224;  Conservative    7;  Mismatches   20;  Indels  247;  Gaps    5;

Qy        120 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEI 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db          1 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETTVEI 60

Qy        180 RIWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQ 239
              ||||||||||||||    |
Db         61 RIWGGIKQLLHILQGSVTF---------------------------------------- 79
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Qy        240 AACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQVINMSLVLQYQV 299
                |
Db         80 ---C---------------------------------------------------------- 80

Qy        300 IEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKY 359
                 :|:||
Db         81 ----------DIYID----------------------------------------------- 85

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419

Db         86 ---------------------------------------------------------- 85

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
                                        ||||||||||||||||||||||||||||||||||||
Db         86 ---------------------DRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 123

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILY 539
                |||||||||||||||||| |||||||||||||||: ||  :|      | :    ||
Db        124 IQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVSSFGDLQQMGVEIMLRNTSQHILP 183

Qy        540 S---CPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKI-------VEAV 589
                |    ||||||||||||||||||||||||||||||||||||||||:       ||||
Db        184 SQKIFPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKVSNAGRQKVEAV 243

Qy        590 YEPVPEGIYSEKVTDTIS 607
                ||||||||||||||||||
Db        244 YEPVPEGIYSEKVTDTIS 261
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RESULT 13
US-09-764-868-1168
; Sequence 1168, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1168
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1168

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  Query Match             10.0%;  Score 520;  DB 9;  Length 106;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-25;
  Matches  101;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        312 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGS 371
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db          1 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPXKYIGNYAILDHLGS 60

Qy        372 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 102
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RESULT 14
US-09-764-891-4539
; Sequence 4539, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4539
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-4539

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  Query Match             10.0%;  Score 520;  DB 10;  Length 106;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-25;
  Matches  101;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        312 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGS 371
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db          1 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPXKYIGNYAILDHLGS 60

Qy        372 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 102
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RESULT 15
US-09-764-875-1003
; Sequence 1003, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ02
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1003
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-1003

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  Query Match             10.0%;  Score 520;  DB 11;  Length 106;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-25;
  Matches  101;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        312 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGS 371
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db          1 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPXKYIGNYAILDHLGS 60

Qy        372 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 102
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Search completed: May 10, 2005, 14:51:09
Job time : 155 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 14:40:07 ; Search time 23 Seconds
(without alignments)
4250.271 Million cell updates/sec

Title: PCT-US03-32302-2
Perfect score: 5214
Sequence: 1 MRVLFDESVLPPTVYFKNCS.....FTSNRYHSYPWGTKNHPTKR 1016

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1156	22.2	1895	2	T15881	hypothetical prote
2	440	8.4	338	2	JC7838	Nek6 protein kinas
3	428.5	8.2	699	2	A43734	probable protein k
4	423	8.1	445	2	G01452	NIMA-like protein
5	395.5	7.6	779	2	A57177	NIMA-like protein
6	390.5	7.5	648	2	T47988	serine/threonine-p
7	390.5	7.5	792	2	JC7122	protein kinase (EC
8	387.5	7.4	722	2	T37970	probable G2-specif
9	385	7.4	774	2	S25284	protein kinase nek
10	385	7.4	795	2	JC4234	gene fused protein
11	383	7.3	841	1	I78885	serine/threonine-s
12	370.5	7.1	435	2	S23580	probable protein k
13	368	7.1	294	2	T21075	hypothetical prote
14	360.5	6.9	357	2	T29771	hypothetical prote
15	358	6.9	651	2	A96591	NPK1-related prote
16	357	6.8	422	2	T26334	hypothetical prote
17	356	6.8	941	2	T49136	protein kinase-lik
18	355.5	6.8	504	2	T38226	probable serine-th
19	349.5	6.7	901	2	S65161	hypothetical prote
20	348.5	6.7	490	2	S47946	protein kinase hom
21	347.5	6.7	524	2	A45472	protein kinase (EC
22	347.5	6.7	887	2	T20941	hypothetical prote
23	346.5	6.6	532	2	T14335	protein kinase, ca
24	344	6.6	431	2	T11854	protein kinase (EC
25	344	6.6	471	2	S68463	protein kinase ATP
26	344	6.6	1097	2	F96538	hypothetical prote
27	344	6.6	1401	2	T39225	MAP kinase kinase
28	342	6.6	798	2	JC7500	qik protein - chic
29	340.5	6.5	836	2	B96716	probable serine/th
30	339.5	6.5	580	2	T40939	probable Ca-calmod
31	339.5	6.5	683	2	T38254	serine/threonine-s
32	339	6.5	374	1	S50193	Ca2+/calmodulin-de
33	337	6.5	384	2	T41298	ser/thr protein ki
34	335.5	6.4	1379	2	JC5778	apoptosis signal-r
35	335	6.4	370	1	S57347	Ca2+/calmodulin-de
36	333.5	6.4	461	2	T14822	probable serine/th
37	332	6.4	479	2	A38578	protein kinase 2 (
38	332	6.4	746	2	S62365	SNF1-related prote
39	331	6.3	465	2	S68462	protein kinase ATP
40	330	6.3	421	2	A56220	protein kinase (EC
41	330	6.3	602	2	S72513	FOG2 protein - yea
42	328.5	6.3	456	2	T48478	serine/threonine p
43	328	6.3	348	2	T37321	Ca2+/calmodulin-de
44	328	6.3	1387	2	T16511	hypothetical prote
45	327.5	6.3	1064	2	S52687	serine/threonine-s

ALIGNMENTS

RESULT 1
T15881
hypothetical protein D1044.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15881
R;Pauley, A.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z18423
A;Accession: T15881
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1895 <PAU>
A;Cross-references: EMBL:U00065; NID:g495681; PID:g495684; PIDN:AAA50735.1; CESP:D1044.
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:D1044.3
A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 1

Query Match 22.2%; Score 1156; DB 2; Length 1895;
Best Local Similarity 30.4%; Pred. No. 5.7e-39;
Matches 312; Conservative 184; Mismatches 296; Indels 236; Gaps 31;

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Qy          13 TVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH----TVDKLVNM 68
               |  ::||                                |  : :|: :|     :|    ||   :|:
Db         116 TKSYRNCK--------------------FQTFQFIASRFL---RSEHDWNVTVVNCLNV 151

Qy          69 TYIFQKLA-AVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE--------R 119
               |   |||    :: |::|  :     || ||  |   ||  ||  |  |::
Db         152 T---QKLIDNGENARKFVDCNLEDAVLV-LLATRQMTVLQHSLEILGRLSDWSTTCRENL 207

Qy         120 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEI 179
               |   |||:|  | | :||:::|:|:| || ||   : :| | : | | |: |  |||:||
Db         208 LCISLLRILSCEEQAREQIRIYDGVPTLLGLLSIKNSRLQWHVAWTLAQLAEQHETSLEI 267

Qy         180 RIWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQ 239
               |||  :                          ||       :|    | :  :  ::
Db         268 AQLGGISLIF----------------------AA-------ISNPKPPGKAVGDWVAML 297

Qy         240 AACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKS----NLLQV-INMSLV 294
               | | :|    :|   :   ||||  : ||:   |     ::    :|||  |   |
Db         298 TGLTALLAQLAQASSNQQLMSNANGVYILGKLLAIKKNVTTDETIDSWDLLQCSIFRVLR 357

Qy         295 LQY------QVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIE 348
               | |      |::: :   ::|| |:|:|:|   :: |:::    : |:|: : :| :: |
Db         358 LMYTFERSRQLLKKVLPTEIPEKFVDVGNYNSVLTDYDQIAKMYDNLIEENI-EIMKDWE 416

Qy         349 SINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRK----HSGQ--NLLAMKEVNLHNPAFG 402
               ::|: :  :  :| | :|| ||:|||||| |||    ||     |||:||: : |
Db         417 TVNERRQAVGEVGEYELLDQLGAGAFGCVYTVRKKAQSHSENPAKLLALKEIFMTN---- 472
```

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Qy        403 KDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSS 462
Db        473 LNDRESDKSFGDMISEVKIIKQQLRHPNIVRYRRIFVENHRLYIVMDLIQGCSLRDLIIT 532

Qy        463 LKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK 522
Db        533 MKEKKGNFEEKKIWAMVVQMMLALRYLHKEKQIVHRDLKPNNIMMTTDERVVITDFGLAK 592

Qy        523 QKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLA 582
Db        593 QKGP-EYLKSAAGTIIYSCPEIVQNLPYGEKADIWSFGCCIYEMCQLQPVFHSTNMLTLA 651

Qy        583 TKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQ 642
Db        652 MQIVEAKYDPLNE-MWSDDLRFLITSCLAPDPSARPDILKVSGMCGVRLLEYLDDVARQQ 710

Qy        643 LSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELS 702
Db        711 ----------------------------------------------ASTSDMTAS------ 719

Qy        703 ESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSS 762
Db        720 ----------QSSY----------------------------NIKIDESPSSLNSSTS 739

Qy        763 PLKESTFNILKRSFSASGGER-----QSQTRDFTGGTGSRPRPA---LLP-----LDLLL 809
Db        740 SYKRP-----GRSSKTSGSGKLPPINPAPRRNHSMSAGETPRPSSIVCLPRITDKYSVMF 794

Qy        810 KVPPHML--RAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQR 867
Db        795 PSAPSAIPSRRRVQTCSTE-------HPARSSSSTELK---------VSKQSDGLTVSSN 838

Qy        868 KVRQISDPIQQILIQLHKIIYITQ---LPPALHHNLKRRVIERFKKSLFSQQSNPCNLKS 924
Db        839 VLRQIQDPVLTILNQIHRILVVTDKETISTSMNH--QRRLVEMFRKNLLGRENDAVQMKT 896

Qy        925 EIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQTV 984
Db        897 HLRKLAAESPEEIQMNLGFSDFRPVLVQSHINGYQKDQKV---------TKITYEQLSAC 947

Qy        985 IEEVLEES 992
Db        948 IECLIAEN 955
```

RESULT 2
JC7838
Nek6 protein kinase, NIMA histone H3 kinase homolog - human
C;Species: Homo sapiens (man)
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C;Accession: JC7838
R;Hashimoto, Y.; Akita, H.; Hibino, M.; Kohri, K.; Nakanishi, M.
Biochem. Biophys. Res. Commun. 293, 753-758, 2002
A;Title: Identification and characterization of Nek6 protein kinase, a potential human h
A;Reference number: JC7838; MUID:22050088; PMID:12054534
A;Accession: JC7838
A;Molecule type: mRNA
A;Residues: 1-338 <HAS>
A;Cross-references: UNIPROT:Q9HC98; DDBJ:AB026289
C;Comment: This protein, a novel member of NIMA (never in mitosis, gene A) related kinas
 playing a conserved central role in regulating mitotic chromosome condensation and asse
C;Genetics:
A;Gene: nek6
A;Map position: 9q33-34

  Query Match   8.4%; Score 440; DB 2; Length 338;
  Best Local Similarity   34.8%; Pred. No. 3.7e-11;
  Matches   92; Conservative   54; Mismatches 106; Indels   12; Gaps   5;

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Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
Db         67 LADFQIEKKIGRGQFSEVYKATCLLDRKTVALKKVQIFEMMDAKARQD-------CVKEI 119

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
Db        120 GLLK-QLNHPNIIKYLDSFIEDNELNIVLELADAGDLSQMIKYFKKQKRLIPERTVWKYF 178

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK-QKQENSKLTSVVGTIL 538
Db        179 VQLCSAVEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLGRFFSSETTAAHSLVGTPY 237

Qy        539 YSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVPEG 596
Db        238 YMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLFSLCQKIEQCDYPPLPGE 297

Qy        597 IYSEKVTDTISRCLTPDAEARPDI 620
Db        298 HYSEKLRELVSMCICPDPHQRPDI 321
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RESULT 3
A43734
probable protein kinase nimA (EC 2.7.1.-) - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A43734; S28786
R;Osmani, S.A.; Pu, R.T.; Morris, N.R.
Cell 53, 237-244, 1988
A;Title: Mitotic induction and maintenance by overexpression of a G2-specific gene that
A;Reference number: A43734; MUID:88194523; PMID:3359487
A;Accession: A43734
A;Molecule type: DNA
A;Residues: 1-699 <OSM>
A;Cross-references: UNIPROT:P11837; GB:M20249; NID:g168065; PIDN:AAA33316.1; PID:g168066
C;Genetics:
A;Gene: nimA
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C;Keywords: ATP; autophosphorylation; nucleus; phosphoprotein; phosphotransferase; serin
F;9-295/Domain: protein kinase homology <KIN>
F;17-25/Region: protein kinase ATP-binding motif

  Query Match   8.2%; Score 428.5; DB 2; Length 699;
  Best Local Similarity   26.9%; Pred. No. 2.4e-10;
  Matches 119; Conservative   80; Mismatches 176; Indels   67; Gaps   12;

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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422
Db         11 YEVLEKIGCGSFGIIRKVKRKSDGFILCRKEINY----IKMSTKERE----QLTAEFNIL 62

Qy        423 KEQLYHPNIVRYY--KTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFI 480
Db         63 -SSLRHPNIVAYYHREHLKASQDLYLYMEYCGGGDLSMVIKNLKRTNKYAEEDFVWRILS 121

Qy        481 QLCLALRYLH----------------------------KEKRIVHRDLTPNNIMLGDKDKVT 514
Db        122 QLVTALYRCHYGTDPAEVGSNLLGPAPKPSGLKGKQAQMTILHRDLKPENIFLGSDNTVK 181

Qy        515 VTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY 574
Db        182 LGDFGLSKLMHSHDFASTYVGTPFYMSPEICAAEKYTLRSDIWAVGCIMYELCQREPPFN 241

Qy        575 STNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKY 634
Db        242 ARTHIQLVQKIREGKFAPLPD-FYSSELKNVIASCLRVNPDHRPD---TATLINTPVIRL 297

Qy        635 ------LDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE-KASL 687
Db        298 MRREVELNNLSRAARKREEATMQKAKDVEQAFAKLEKEKQQIRSELENSIRREWEVKARL 357

Qy        688 SSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVD 747
Db        358 --------EIDRQVQNELDKLRKRFECEV---QDRVAQEV--------EKQRRNANYRED 398

Qy        748 DELDISDNSSSSSSSPLKESTF 769
Db        399 ASLRSSGHSSQMSSSNSEDSDF 420
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RESULT 4
G01452
NIMA-like protein kinase 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01452
R;Lu, K.P.
submitted to the EMBL Data Library, June 1994
A;Reference number: G07172
A;Accession: G01452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-445 <LUX>
A;Cross-references: UNIPROT:P51955; EMBL:U11050; NID:g507874; PIDN:AAA19558.1; PID:g5078
C;Genetics:
A;Gene: NLK1
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;6-271/Domain: protein kinase homology <KIN>
F;14-22/Region: protein kinase ATP-binding motif

Query Match 8.1%; Score 423; DB 2; Length 445;
Best Local Similarity 27.8%; Pred. No. 2.4e-10;
Matches 125; Conservative 90; Mismatches 170; Indels 64; Gaps 15;

```
Qy        362 NYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTI 421
              :| :|  :|:|::|   |:|: |   :|  ||::  :          ::  : :|||: :
Db          7 DYEVLYTIGTGSYGRCQKIRRKSDGKILVWKELDYGSMT--------EAEKQMLVSEVNL 58

Qy        422 IKEQLYHPNIVRYYKTFLE--NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| | ||||||||   ::  |  ||||||  ||  |    :  ::  :  || : ::
Db         59 LRE-LKHPNIVRYYDRIIDRTNTTLYIVMEYCEGGDLASVITKGTKERQYLDEEFVLRVM 117

Qy        480 IQLCLALRYLHKEK----RIVHRDLTPNNIMLGDKDKVTVTDFGLAK-QKQENSKLTSVV 534
               || |||:  |:       ::|||| | |: |  |  | : |||||:    : |   : |
Db        118 TQLTLALKECHRRSDGGHTVLHRDLKPANVFLDGKQNVKLGDFGLARILNHDTSFAKTFV 177

Qy        535 GTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVP 594
              ||  |  || :    | ||:|:|::||:||::  | ||| : :   || || |  :  :|
Db        178 GTPYYMSPEQMNRMSYNEKSDIWSLGCLLYELCALMPPFTAFSQKELAGKIREGKFRRIP 237

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEV--SSMISDVMMKYLDNLSTSQLSLEKKLERE 652
                ||::: : |:| |      || : |:  : :|:|::             |::   |
Db        238 YR-YSDELNEIITRMLNLKDYHRPSVEEILENPLIADLVAD-----------EQRRNLE 284

Qy        653 RRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGF 712
              ||  |    | ::::        |||    ::  |        : :  | :
Db        285 RRGRQLGEPEKSQDS------SPVLSELKLKEIQLQERERALKAREERLEQ--------- 329

Qy        713 QASYGKDEDRACDEILSDDNF-NLENAEKDTYSEVDDE--LDISDNSS--SSSSSPLK-- 765
                  |:::    | |::|      ||  |: || : :   | :: |    :  || :|
Db        330 -----KEQELCVRERLAEDKLARAENLLKN-YSLLKERKFLSLASNPELLNLPSSVIKKK 383

Qy        766 -----ESTFNILKRSFSASGGERQSQTRD 789
                  ||  ||::   | |    :|: :|
Db        384 VHFSGESKENIMRSENSESQLTSKSKCKD 412
```

RESULT 5
A57177
NIMA-like protein kinase - Neurosproa crassa
C;Species: Neurosproa crassa
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 11-Aug-2003
C;Accession: A57177
R;Pu, R.T.; Xu, G.; Wu, L.; Vierula, J.; O'Donnell, K.; Ye, X.S.; Osmani, S.A.
J. Biol. Chem. 270, 18110-18116, 1995
A;Title: Isolation of a functional homolog of the cell cycle-specific NIMA protein kinas
A;Reference number: A57177; MUID:95355415; PMID:7629122
A;Accession: A57177
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-779 <PUA>
A;Cross-references: GB:L42573; NID:g1040682; PIDN:AAA80145.1; PID:g1040683
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C;Keywords: ATP
F;5-290/Domain: protein kinase homology <KIN>
F;13-21/Region: protein kinase ATP-binding motif

Query Match 7.6%; Score 395.5; DB 2; Length 779;
Best Local Similarity 25.5%; Pred. No. 5.7e-09;
Matches 130; Conservative 83; Mismatches 198; Indels 99; Gaps 17;

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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422
              | :|: :| |:|| : |||: :   :|  ||::         :|:|:     : :| :|:
Db          7 YELLEKIGHGSFGIIRKVRRKADGMILCRKEISY----LKMSQKERE----QLHAEFSIL 58

Qy        423 KEQLYHPNIVRYY--KTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFI 480
              | ||||| ||  :       |:: ||       ||    :| : : :  |  :| ||
Db         59 -STLRHPNIVGYYHREHLKATQDLHLYMEYCGNGDLGRVIRNLIKNNQYAEESFVWSIFS 117

Qy        481 QLCLALRYLH-------------------KEK------RIVHRDLTPNNIMLGDKDKVTV 515
              ||  ||  |                     : |       |:|||| | |: ||: : | :
Db        118 QLVTALYRCHYGVDPPEVGKTVLGLGSTARPKPPSGGMTILHRDLKPENVFLGEDNSVKL 177

Qy        516 TDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYS 575
              ||||:|  | :   :: |||  |  ||:  :| |  |:|:|::|||:|::    ||| :
Db        178 GDFGLSKVMQSHDFASTYVGTPFYMSPEICAAEKYTLKSDIWSLGCIIYELCAREPPFNA 237

Qy        576 TNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPD---------------- 619
                  |  || |    |:|  :|| ::  ||  ||  : : |||
Db        238 KTHYQLVQKIKEGKIAPLP-SVYSGELFATIKDCLRVNPDRRPDTATLLNLPIVRLMRKE 296

Qy        620 --IVEVSSMIS------DVMMKYLDN----LSTSQLSLEKKLERERRRTQRYFMEANRNT 667
                :|| |  :       :  :: ||:    | | : |:  :::   ||
Db        297 KEVVEFSRTLRTKEETLNKRIRELDSKLSALETEKSSIRAEIDASLRREWE--------- 347

Qy        668 VTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLP---PEGFQASYGKDEDRAC 724
              |    |:  |  :  |             | :::||      |     | | |:
Db        348 VKARLEIDRLVAQEIESLQQKFEQEVQARVEAELQRHGRGPMFNSHGQQGSFSS----TA 403

Qy        725 DEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQ 784
              ::|| | :   :    :    |  |||   |:  |    :  | |  :  |      :
Db        404 ATLVSDYNLSSVGSGDGDFPSTTDITDISIAESSTDGS----DITKKIPRTPF------HR 453

Qy        785 SQTRDFTGGTGSRPRPALL--PLDLLLKVP 812
              :||       | |  ::|  |:|: :  |
Db        454 AQT------YSSAPAESVLGTPMDIEMASP 477
```

RESULT 6
T47988
serine/threonine-protein kinase-like protein - Arabidopsis thaliana
N;Alternate names: protein F21F14.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47988
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; S
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24481
A;Accession: T47988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-648 <CHO>
A;Cross-references: UNIPROT:Q9M269; EMBL:AL138642
A;Experimental source: cultivar Columbia; BAC clone F21F14
C;Genetics:
A;Map position: 3
A;Introns: 77/3; 117/1; 136/3; 158/2; 189/3; 216/3; 254/1; 272/2; 483/3; 563/1; 586/3
A;Note: F21F14.130

Query Match 7.5%; Score 390.5; DB 2; Length 648;
Best Local Similarity 24.3%; Pred. No. 7.4e-09;
Matches 173; Conservative 111; Mismatches 236; Indels 193; Gaps 32;

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Qy        358 KYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR-NIV 416
Db          5 RLVGDYALGPRIGSGSFAVVWLAKHRSSGLEVAVKEI---------DKKLLSPKVRDNLL 55

Qy        417 SELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLW 476
Db         56 KEISIL-STIDHPNIIRFYEAIETGDRIFLVLEYCSGGDLAGYIN-----RHGKVPEAVA 109

Qy        477 KIFI-QLCLALRYLHKEKRIVHRDLTPNNIMLGDKD---KVTVTDFGLAKQKQENSKLTS 532
Db        110 KHFMRQLALGLQVL-QEKHFIHRDLKPQNLLLSSKEVTPLLKIGDFGFARSLTPESMAET 168

Qy        533 VVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEP 592
Db        169 FCGSPLYMAPEIIRNQKYDAKADLWSAGAILFQLVTGKPPFDGNNHIQLFHNIVRDTELK 228

Qy        593 VPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERE 652
Db        229 FPE--------DTRN-------EIHPDCVDLCR-----------------SLLRRNPIE 255

Qy        653 RRRTQRYFMEANRNTVTCHHELAVLSHETFEKA---SLSSSSSGAASLKSELSESADLPP 709
Db        256 RLTFREFF---NHMFLREPRQIPDVEHSGFSTCTGKSLLPSAQPSTSTNRFKSSAENVHK 312

Qy        710 EGFQASYGKDEDRACDEILSDDNFNLENAEKD---------------------------- 741
Db        313 HGSSSS-------ASNSQISMPHTSFEKTRKDTEGQCSSNQSGGLLFAILCLISVALYKI 365

Qy        742 ---TYS-----EVDDELDI-------------SDNSSSSSSSPLKESTF-NILKRS--F 776
Db        366 VLLTYSCYVIRAVVDSLELIEREYVLVNRPSASLEGSSDCFDTSLQDSGFPNILPRNEKV 425

Qy        777 SASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKV-------PPHMLRAHIKEIEA--EL 827
Db        426 SSSSLEAQKPLSDVSG-----PRPASVSY-LLTEVQRLTIVHPPTKLQLLHQYAQALTEL 479

Qy        828 VTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGI------AVSQRKVRQISDPIQQILI 881
Db        480 ASEMESFAVTLVVLA-----------VWRKALEICDSWMMSVGENEVN--PDP------ 519

Qy        882 QLHKIIYITQLPPALHHNL------KRRVIERFKKSLFSQQSNPCNLKSEIKKLSQGS-- 933
Db        520 --------TTAPETSIPDLNSPAPAKTWVTQEFVTALNQAE----NLSTQLNETSAATHM 567

Qy        934 PEPIEPNFFTADYHLLHRSSGG--NSLSPNDPTG-------LPTSIELEEGIT 977
Db        568 PDAMETIYERA---LAYGKSGGAEEYLSNKESAATLYKKAILLLSFIIEEAVT 617
```

RESULT 7
JC7122
protein kinase (EC 2.7.1.37) 2 - mouse (strain balb/c)
N;Alternate names: serine (threonine) protein kinase
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: JC7122
R;Hayashi, K.; Igarashi, H.; Ogawa, M.; Sakaguchi, N.
Biochem. Biophys. Res. Commun. 264, 449-456, 1999
A;Title: Activity and substrate specificity of the murine STK2 serine/threonine kinase t
A;Reference number: JC7122; MUID:20001940; PMID:10529384
A;Accession: JC7122
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-792 <HAY>
A;Cross-references: UNIPROT:Q9Z1J2; GB:AJ223071; NID:g4138208; PID:g4138209
C;Genetics:
A;Gene: MSTK2L
C;Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C;Keywords: phosphotransferase

Query Match 7.5%; Score 390.5; DB 2; Length 792;
Best Local Similarity 27.6%; Pred. No. 9.3e-09;
Matches 135; Conservative 78; Mismatches 181; Indels 95; Gaps 20;

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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422
Db          6 YCYMRVVGRGSYGEVTLVKHRRDGKQYVIKKLNLRNAS---------SRERRAAEQEAQL 56

Qy        423 KEQLYHPNIVRYYKTFLEND-RLYIVMELIEGAPLGEHFSSLKE-KHHHFTEERLWKIFI 480
Db         57 LSQLKHPNIVTYKESWEGGDGLLYIVMGFCEG---GDLYRKLKEQKGQLLPESQVVEWFV 113

Qy        481 QLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTS-VVGTILY 539
Db        114 QIAMALQYLH-EKHILHRDLKTQNVFLTRTNIIKVGDLGIARVLENHGDMASTLIGTPYY 172

Qy        540 SCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYS 599
Db        173 MSPELFSNKPYNYKSDVWALGCCVYEMATLKHAFNAKDMNSLVYRIIEGKLPPMPK-VYS 231

Qy        600 EKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRY 659
Db        232 TELAELIRTMLSRRPEERP---SVRSILRQPYIKH-------HISL--FLEATKAKTSK- 278

Qy        660 FMEANRNTVTCHHE----LAVLSHETFEKASL------SSSSSGAASLKSELSESADLP- 708
Db        279 -----NNVKNCDSRAKPVAAVVSRKEESNTDVIHYQPRSSEGSALHVMGEDKCLSQEKPV 333

Qy        709 -------PEGFQASYGKDEDRACDE---ILSDDNFNLENAEK----------------D 741
Db        334 DIGPLRSPASLEGHTGKQDMNNTGESCATISRINIDILPAERRDSANAGVVQESQPQHVD 393

Qy        742 TYSEVDDELDIS------DNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTG 795
Db        394 AADEVDSQCSISQEKERLQGNTKSSDQP-----GNLLPRR-SSDGGD----------GEG 437

Qy        796 SRPRPALLP 804
Db        438 SELVKPLYP 446
```

RESULT 8
T37970
probable G2-specific protein kinase (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pc
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T37970
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21758
A;Accession: T37970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-722 <BAD>
A;Cross-references: UNIPROT:O13839; EMBL:Z98975; PIDN:CAB11653.1; GSPDB:GN00066; SPDB:S
A;Experimental source: strain 972h-; cosmid c19E9
C;Genetics:
A;Gene: SPDB:SPAC19E9.02
A;Map position: 1
A;Introns: 20/3; 28/3
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase; protein kinase

Query Match 7.4%; Score 387.5; DB 2; Length 722;
Best Local Similarity 23.4%; Pred. No. 1.1e-08;
Matches 156; Conservative 91; Mismatches 228; Indels 193; Gaps 25;

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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422
Db          4 YKILECIGHGSFGRIYKVQRLKDGALLAQKEIHFGN--ITRQEK------QYIADEVNIL 55

Qy        423 KEQLYHPNIVRYYKTFLENDR--LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFI 480
Db         56 R-NLKHPNIVQYCGEELNRSAQVINLYMEYCGHGDLANLIQRYKEEKKRFTEQEVLKFFT 114

Qy        481 QLCLAL-----------------RYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK 522
```

```
Db        115 QLLLALYRCHYGENAPACDSQWPREIFHPKQSVLHRDIKPANIFLDENNSVKLGDFGLSK 174

Qy        523 QKQENSKLT-SVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSL 581

Db        175 LLDNTRVFTQSYVGTPYYMSPEIIRSSPYSAKSDVWALGCVIFEICMLTHPFEGRSYLEL 234

Qy        582 ATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV--SSMISDVMMKYLDNLS 639

Db        235 QRNICQGNLS-CWDHHYSDDVFLLIRHCLEVNSDLRPTTYQLLRSPILSDI--------- 284

Qy        640 TSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHE-TFEKASLSSSSSGAASLK 698

Db        285 -----------RSKLESERVVLEQSDLLHKKHQMLIQLENDLQFREQRLSARES------ 327

Qy        699 SELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSS 758

Db        328 ----------------------------------ELENVIASRLAQREE---------- 342

Qy        759 SSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRA 818

Db        343 -----------ILRR-------ELEKQLRDMDA----------------RYQRHM-QT 365

Qy        819 HIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQ-----IS 873

Db        366 VVNSMQKMRVTSPVDH-----------NEQPESSTAEMFVDCTIEASQSPLLHIPKLGIS 414

Qy        874 DPIQQILIQLHKIIYITQLP----PALHHNLKRRVIE------RFKKSLFSQQSNPCNLK 923

Db        415 KPLQ--TLSCPGFTLTTQQPILKRPTLRKELSSRALHTTATLMKYRANASSLRTTPIDKD 472

Qy        924 SEIKKLSQ--GSPEPIEPNFFTAD--YHLLHRSSGGNSLSP-------NDPTGLPT---- 968

Db        473 GQITSLQQKNGTSNQV------ADCMNKLLHTSLDGKKLSPSELCNKFSDGEGLPNRKVS 526

Qy        969 --SIELEE 974

Db        527 KLSVESDE 534


RESULT 9
S25284
protein kinase nek1 (EC 2.7.1.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C;Accession: S25284
R;Letwin, K.; Mizzen, L.; Motro, B.; Ben-David, Y.; Bernstein, A.; Pawson, T.
EMBO J. 11, 3521-3531, 1992
A;Title: A mammalian dual specificity protein kinase, Nek1, is related to the NIMA cell
A;Reference number: S25284; MUID:93010942; PMID:1382974
A;Accession: S25284
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-774 <LET>
A;Cross-references: UNIPROT:P51954; GB:S45828; NID:g256854; PIDN:AAB23529.1; PID:g256855
C;Genetics:
A;Gene: nek1
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase
F;2-258/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif

  Query Match             7.4%;  Score 385;  DB 2;  Length 774;
  Best Local Similarity   30.8%;  Pred. No. 1.5e-08;
  Matches   88;  Conservative   63;  Mismatches  119;  Indels   16;  Gaps    7;

Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422

Db          4 YVRLQKIGEGSFGKAVLVKSTEDGRHYVIKEINISR----MSDKERQESRREVA-----V 54

Qy        423 KEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQL 482

Db         55 LANMKHPNIVQYKESFEENGSLYIVMDYCEGGDLFKRINA--QKGALFQEDQILDWFVQI 112

Qy        483 CLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT-SVVGTILYSC 541

Db        113 CLALKHVH-DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLS 171

Qy        542 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 601

Db        172 PEICENKPYNNKSDIWALGCVLYELCTLKHAFEAGNMKNLVLKIISGSFPPVSPH-YSYD 230

Qy        602 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEK 647

Db        231 LRSLLSQLFKRNPRDRPSVNSI--LEKGFIAKRIEKFLSPQLIAEE 274


RESULT 10
JC4234
gene fused protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 16-Aug-2004
C;Accession: JC4234
R;Blanchet-Tournier, M.F.; Tricoire, H.; Busson, D.; Lamour-Isnard, C.
Gene 161, 157-162, 1995
A;Title: The segment-polarity gene fused is highly conserved in Drosophila.
A;Reference number: JC4234; MUID:95394348; PMID:7665071
A;Accession: JC4234
A;Molecule type: DNA
A;Residues: 1-795 <BLA>
A;Cross-references: GB:U20586; NID:g1079514; PIDN:AAA82044.1; PID:g1079515
C;Comment: This protein belongs to the segment polarity class of the segmentation. It m
e signalling of wing-less-expressing cells by the Hedgehog extracellular protein.
C;Genetics:
A;Gene: fu
A;Cross-references: FlyBase:FBgn0001079
A;Introns: 37/3; 287/2; 485/2; 675/3
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphoprotein; segmentation
F;2-254/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;427/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predi
F;450/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predi

  Query Match             7.4%;  Score 385;  DB 2;  Length 795;
  Best Local Similarity   23.2%;  Pred. No. 1.5e-08;
  Matches  165;  Conservative  119;  Mismatches  240;  Indels  186;  Gaps   30;

Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDS-SVRNIVSELTI 421

Db          4 YAVSSLVGQGSFGCVYKAQRRDDDKVVAIKVIS---------KRGRSNRELKNLRRECD- 53

Qy        422 IKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFT------EERL 475

Db         54 IQARLKHPHVIEMVESFESKFDLFVVTEF-----------ALMDLHRYLSFNGAMPEEHA 102

Qy        476 WKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSK-LTSVV 534

Db        103 QRVVCHLVSALYYLH-SNRILHRDLKPQNVLLDKNMHAKLCDFGLARNMTMGTHVLTSIK 161

Qy        535 GTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKI--------- 585

Db        162 GTPLYMAPELLAEQPYDHQADMWSLGCIAYESMAGQPPFCATSILHLVKLIKHEDVKWPS 221

Qy        586 ------------------------VEAVYEPVPEG------IYSEKVTDTISRCLTPDAE 615

Db        222 TLSSECRSFLQGLLEKDPSMRISWTQLLCHPFVEGKLYIAEVQAAQTSPFINPQLAKDTK 281

Qy        616 ARPDIVEVSSMISDVM--MKYLD----NLSTSQLSLE-------KKLERE---------- 652

Db        282 KSQQLRHVGADLGDVLAALKLSDVANENLSTSRDSINAIAPSDIEQLETDVEDNVHRLIV 341

Qy        653 ------------------RR-------RTQRYFMEANRNTVTCHHELAVLSHETFEKASL 687

Db        342 PFADISYRELPCGTAAAARRAGAMPLINSQTCFVSGNSN--------MILNHLNDNFAIE 393
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Qy        688 SSSSSGAASLKSELSESADLPPEGFQASYGKD-EDRACDEILSDDNFNLENAEKDTYSEV 746
Db        394 APASSATKSMKSKLKLALNI-----KQSRSKDLEKRKLSQNL--DNFSLRLGQ-----SI 441

Qy        747 DDELDISDN---SSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALL 803
Db        442 DIEVQRKTTEMLTQQSQAQQLQDRKTQQLKQSMHSTNDEKLS---------SDNSPPCLL 492

Qy        804 P----LDLLLKVPP-------HMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMG 852
Db        493 PGWDSCD-ESQSPPIENDEWLAFLHRSIQELLDGEFDSLKQHNLVSIIVAPLRN------ 545

Qy        853 TFLWQASAGIAVSQRKVRQISDPI----QQILIQLHKIIYI-TQLPPALHHNLKRRVIER 907
Db        546 -----SKAIPKVLQSVAQLLSLPFVLAEQHLVAEAIKGVYIDVKLVPNLMYACKLLLSQR 600

Qy        908 FKKSLFSQQSNPC----NLKSEIKKLSQGSPEPIEP--NFFTADYHLLHR 951
Db        601 HLTD--SAASLPAGTGVSLSRTVRSCSDLSAEEMSTACSLYELVCHLVHQ 648
```

RESULT 11
I78885
serine/threonine-specific protein kinase (EC 2.7.1.-) STK2 - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I78885
R;Levedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simmc
Oncogene 9, 1977-1988, 1994
A;Title: Two novel human serine/threonine kinases with homologies to the cell cycle regu
A;Reference number: I58396; MUID:94268838; PMID:8208544
A;Accession: I78885
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-841 <RES>
A;Cross-references: UNIPROT:P51957; GB:L20321; NID:g348244; PIDN:AAA36658.1; PID:g348245
C;Genetics:
A;Gene: GDB:STK2
A;Cross-references: GDB:374125
A;Map position: 3p21.1-3p21.1
C;Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C;Keywords: phosphotransferase
F;4-261/Domain: protein kinase homology <KIN>

  Query Match 7.3%; Score 383; DB 1; Length 841;
  Best Local Similarity 28.2%; Pred. No. 2e-08;
  Matches 122; Conservative 80; Mismatches 178; Indels 52; Gaps 15;

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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422
Db          6 YCYLRVVGKGSYGEVTLVKHRRDGKQYVIKKLNLRNAS---------SRERRAAEQEAQL 56

Qy        423 KEQLYHPNIVRYYKTFLEND-RLYIVMELIEGAPLGEHFSSLKE-KHHHFTEERLWKIFI 480
Db         57 LSQLKHPNIVTYKESWEGGDGLLYIVMGFCEG---GDLYRKLKEQKGQLLPENQVVEWFV 113

Qy        481 QLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTS-VVGTILY 539
Db        114 QIAMALQYLH-EKHILHRDLKTQNVFLTRTNIIKVGDLGIARVLENHCDMASTLIGTPYY 172

Qy        540 SCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYS 599
Db        173 MSPELFSNKPYNYKSDVWALGCCVYEMATLKHAFNAKDMNSLVYRIIEGKLPAMPRD-YS 231

Qy        600 EKVTDTISRCLTPDAEARPDIVEVSSMISDVMMK-----YLD--NLSTSQLSLEKKLERE 652
Db        232 PELAELIRTMLSKRPEERP---SVRSILRQPYIKRQISFFLEATKIKTSKNNIKNGDSQS 288

Qy        653 RRRTQRYFMEANRNTVTCHHE-LAVLSHETF----------EKASLSSSSSGAASLK--- 698
Db        289 KPFATVVSGEAESNHEVIHPQPLSSEGSQTYIMGEGKCLSQEKPRASGLLKSPASLKAHT 348

Qy        699 -----SELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKD-----TYSEVDD 748
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Db        349 CKQDLSNTTELATISSVNIDILPAKGRDSVSDGFVQENQPRYLDASNELGGICSISQVEE 408

Qy        749 ELDISDNSSSSS 760
Db        409 EM-LQDNTKSSA 419
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RESULT 12
S23580
probable protein kinase KIN3 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: probable protein kinase FUN52; probable protein kinase NPK1; protein
C;Species: Saccharomyces cerevisiae
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 16-Aug-2004
C;Accession: S23580; S20123; S40906; S43451; S11185
R;Schweitzer, B.; Philippsen, P.
Mol. Gen. Genet. 234, 164-167, 1992
A;Title: NPK1, a nonessential protein kinase gene in Saccharomyces cerevisiae with simil
A;Reference number: S23580; MUID:92357012; PMID:1495480
A;Accession: S23580
A;Molecule type: DNA
A;Residues: 1-435 <SCH>
A;Cross-references: UNIPROT:P22209; EMBL:X60549; NID:g298024; PIDN:CAA43042.1; PID:g2980
R;Davies, C.J.; Hutchison III, C.A.
submitted to the EMBL Data Library, January 1992
A;Description: A directed DNA sequencing strategy based upon Tn3 transposon mutagenesis
A;Reference number: S20123
A;Accession: S20123
A;Molecule type: DNA
A;Residues: 1-435 <DAV>
A;Cross-references: EMBL:M67445
R;Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Oue
submitted to the EMBL Data Library, November 1993
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the 4
A;Reference number: S40891
A;Accession: S40906
A;Molecule type: DNA
A;Residues: 1-430 <CLA>
A;Cross-references: EMBL:L22015; MIPS:YAR018c
R;Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Oue
Yeast 10, 535-541, 1994
A;Title: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp
A;Reference number: S43441; MUID:95028152; PMID:7941740
A;Accession: S43451
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-435 <CLW>
A;Cross-references: EMBL:L22015; NID:g1339990; PIDN:AAC04964.1; PID:g349756
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
R;Jones, D.G.L.; Rosamond, J.
Gene 90, 87-92, 1990
A;Title: Isolation of a novel protein kinase-encoding gene from yeast by oligodeoxyribor
A;Reference number: S11185; MUID:90337351; PMID:2199332
A;Accession: S11185
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-97,'L',99-120,'Q',122-129,'I',131-234,'SQIS',239-357,'R',359-369 <JON>
A;Cross-references: EMBL:M55416
A;Experimental source: strain SB303
C;Genetics:
A;Gene: SGD:KIN3; NPK1; FUN52
A;Cross-references: SGD:S0000071; MIPS:YAR018c
A;Map position: 1R
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;23-343/Domain: protein kinase homology <KIN>
F;31-39/Region: protein kinase ATP-binding motif

  Query Match 7.1%; Score 370.5; DB 2; Length 435;
  Best Local Similarity 27.0%; Pred. No. 3e-08;
  Matches 117; Conservative 60; Mismatches 143; Indels 113; Gaps 17;

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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFG-KDKKDRDSSVRNIVSELTI 421
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Db         25 YQVLEEIGRGSFGSVRKVIHIPTKKLLVRKDIK-----YGHMNSKER----QQLIAECSI 75

Qy        422 IKEQLYHPNIVRYYKTFLENDR--LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479

Db         76 L-SQLKHENIVEFYNWDFDEQKEVLYLYMEYCSRGDLSQMIKHYKQEHKYIPEKIVWGIL 134

Qy        480 IQLCLALRYLH-------------------KEKRIV-HRDLTPNNIMLGDKDK------- 512

Db        135 AQLLTALYKCHYGVELPTLTTIYDRMKPPVKGKNIVIHRDLKPGNIFLSYDDSDYNINEQ 194

Qy        513 --------------------------------VTVTDFGLAKQKQENSKL-TSVVGTILY 539

Db        195 VDGHEEVNSNYYRDHRVNSGKRGSPMDYSQVVVKLGDFGLAKSLETSIQFATTYVGTPYY 254

Qy        540 SCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYS 599

Db        255 MSPEVLMDQPYSPLSDIWSLGCVIFEMCSLHPPFQAKNYLELQTKIKNGKCDTVPE-YYS 313

Qy        600 EKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRY 659

Db        314 RGLNAIIHSMIDVNLRTRPSTFE---LLQDIQIR------TARKSLQ--LERFERKLLDY 362

Qy        660 FME-------ANRNTVTCHHELAVLSHETFEKA-------SLSSSSSGAASLKSELSESA 705

Db        363 ENELTNIEKILEKQAIEYERELSQLK-EQFTQAVEERAREVISGKKVGKV---------- 411

Qy        706 DLPPEGFQASYGK 718

Db        412 ---PESINGYYGK 421


RESULT 13
T21075
hypothetical protein F19H6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21075; T21124
R;McMurray, A.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19368
A;Accession: T21075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <WIL>
A;Cross-references: UNIPROT:Q19530; EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone F17E5
R;McMurray, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19378
A;Accession: T21124
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <WI2>
A;Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN00028; CESP:F19H6.1
A;Experimental source: clone F19H6
C;Genetics:
A;Gene: CESP:F19H6.1
A;Map position: X
A;Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C;Superfamily: kinase-related transforming protein; protein kinase homology

  Query Match             7.1%;  Score 368;  DB 2;  Length 294;
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Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422

Db         23 FIIEKKIGKGQFSEVFRAQCTWVDLHVALKKIQVFEMV---DQKAR----QDCLKEIDLL 75

Qy        423 KEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQL 482

Db         76 K-QLNHVNVIRYYASFIDNNQLNIVLELAEAGDMSRMIKHFKKGGRLIPEKTIWKYFVQL 134

Qy        483 CLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGTILY 539

Db        135 ARALAHMH-SKRIMHRDIKPANVFITGNGIVKLGDLGLG--RFFSSKTTAAHSLVGTPYY 191

Qy        540 SCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVPEGI 597

Db        192 MSPERIQESGYNFKSDLWSTGCLLYEMAALQSPFYGDKMNLYSLCKKIENCEYPPLPADI 251

Qy        598 YSEKVT 603

Db        252 YSTQVS 257


RESULT 14
T29771
hypothetical protein ZC581.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29771
R;Waterston, B.; Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid ZC581.
A;Reference number: Z20682
A;Accession: T29771
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-357 <WAT>
A;Cross-references: UNIPROT:O01775; EMBL:AF003134; PIDN:AAB54139.1; GSPDB:GN00019; CESP
A;Experimental source: strain Bristol N2; clone ZC581
C;Genetics:
A;Gene: CESP:ZC581.1
A;Map position: 1
A;Introns: 31/3; 81/1; 120/3; 186/1; 226/3; 260/1; 288/3

  Query Match             6.9%;  Score 360.5;  DB 2;  Length 357;
  Best Local Similarity   31.1%;  Pred. No. 6e-08;
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Qy        362 NYAILDHLGSGAFGCVYKVR--KHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419

Db          3 NYEKVRVVGRGAFGVCWLCRGKNDASHQKVIIKLINTH----GMTEKEENS----IQSEV 54

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFS---SLKEKH--HHFTEER 474

Db         55 NLLK-KVQHPLIIGYIDSFIMDNQLGIVMQYAEGGTLERLINDQRAIKDSNMREYFPEKT 113

Qy        475 LWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKV-TVTDFGLAKQKQENSKLTSV 533

Db        114 VLDYFTQILIALNHMH-QKNIVHRDLKPQNILMNRRKTVLKLSDFGISKELGTKSAASTV 172

Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593

Db        173 IGTPNYLSPEICESRPYNQKSDMWSLGCVLYELLQLERAFDGENLPAIVMKITRSKQNPL 232

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISD-VMMKYL 635

Db        233 GDHV-SNDVKMLVENLLKTHTDKRPD---VSQLLSDPLVLPYL 271


RESULT 15
A96591
NPK1-related protein kinase 2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A96591
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
```

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <STO>
A;Cross-references: UNIPROT:Q9FZ36; GB:AE005173; NID:g9857521; PIDN:AAG00876.1; GSPDB:GN
C;Genetics:
A;Gene: T24C10.7
A;Map position: 1
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 6.9%; Score 358; DB 2; Length 651;
Best Local Similarity 26.4%; Pred. No. 1.5e-07;
Matches 123; Conservative 76; Mismatches 179; Indels 88; Gaps 16;

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Qy        352 QNKAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSS 411
              | | |:::     |    | |||| ||          |||:|:| : :    |:|    :
Db         61 QIKPPIRWRKGQLI----GRGAFGTVYMGMNLDSGELLAVKQVLITSNCASKEK--TQAH 114

Qy        412 VRNIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFT 471
              :: :  |: ::|  | |||||||  |  |:: | |::| : |  :    ||| ||   |
Db        115 IQELEEEVKLLK-NLSHPNIVRYLGTVREDETLNILLEFVPGGSI----SSLLEKFGAFP 169

Qy        472 EERLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT 531
              |  :    || | | |||    |:|||:   ||:: ::  : : ||| :||  | : ::
Db        170 ESVVRTYTNQLLLGLEYLHNH-AIMHRDIKGANILVDNQGCIKLADFGASKQVAELATIS 228

Qy        532 ---SVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEA 588
                |: ||  :  |||:    :   ||:|:||| : :| |   |:      |   | : |
Db        229 GAKSMKGTPYWMAPEVILQTGHSFSADIWSVGCTVIEMVTGKAPW------SQQYKEIAA 282

Qy        589 VYE--------PVPEGIYSEKVTDTISRCLTPDAEARPDIVEV----------SSMISDV 630
              ::         |:|: | |:   | : :||  :   ||   |:                |
Db        283 IFHIGTTKSHPPIPDNISSD-ANDFLLKCLQQEPNLRPTASELLKHPFVTGKQKESASKD 341

Qy        631 MMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSS 690
              :  ::|| | | |  |                          |:: |  : | |
Db        342 LTSFMDN-SCSPLPSE----------------------------LTNITSYQTSTSDD 370

Qy        691 SSGAASLKSELSESADLPPEGFQ-------ASYGKDEDRACDEILSDD-NFNLENAEKDT 742
                :| | |: :   | :  |        :: | |:|   |  | || ||   | |
Db        371 VGDICNLGS-LTCTLAFPEKSIQNNSLCLKSNNGYDDDDDNDMCLIDDENFLTYNGETGP 429

Qy        743 YSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTR 788
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Db        430 --------SLDNNTDAKKSCDTMSEISDILKCKFDENSGNGETETK 467
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Search completed: May 10, 2005, 14:48:03
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 14:31:39 ; Search time 183 Seconds
(without alignments)
2843.019 Million cell updates/sec

Title: PCT-US03-32302-2
Perfect score: 5214
Sequence: 1 MRVLFDESVLPPTVYFKNCS.....FTSNRYHSYPWGTKNHPTKR 1016

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2451	47.0	484	2	Q96MB3	Q96mb3 homo sapien
2	2413	46.3	712	2	Q6ZWH5	Q6zwh5 homo sapien
3	2376	45.6	474	2	Q86XB1	Q86xb1 homo sapien
4	2276	43.7	651	2	Q7Z671	Q7z671 homo sapien
5	2057	39.5	404	2	Q8N774	Q8n774 homo sapien
6	1156	22.2	959	1	NEK1_CAEEL	P84199 caenorhabdi
7	1156	22.2	1576	1	YLK3_CAEEL	P41951 caenorhabdi
8	456	8.7	297	2	Q6DEH7	Q6deh7 brachydanio
9	454	8.7	284	2	Q7T001	Q7t001 brachydanio
10	450.5	8.6	580	2	Q6BVX7	Q6bvx7 debaryomyce
11	445	8.5	313	1	NEK6_MOUSE	Q9es70 mus musculu
12	444.5	8.5	442	2	Q6DII1	Q6dii1 xenopus tro
13	444	8.5	310	2	Q6DIX9	Q6dix9 xenopus tro
14	443	8.5	299	2	Q8T755	Q8t755 branchiosto
15	442	8.5	310	2	Q7ZSX4	Q7zsx4 xenopus lae
16	440	8.4	306	2	Q6FG86	Q6fg86 homo sapien
17	440	8.4	313	1	NEK6_HUMAN	Q9hc98 homo sapien
18	440	8.4	442	2	Q9W622	Q9w622 xenopus lae
19	439.5	8.4	367	2	Q7R1M1	Q7r1m1 giardia lam
20	438	8.4	302	1	NEK7_HUMAN	Q8tdx7 homo sapien
21	437	8.4	313	1	NEK6_RAT	P59895 rattus norv
22	437	8.4	442	2	Q7ZYE3	Q7zye3 xenopus lae
23	436	8.4	306	2	Q6IAR3	Q6iar3 homo sapien
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25	434.5	8.3	735	2	Q9W3N8	Q9w3n8 drosophila
26	432	8.3	525	2	Q6UPR2	Q6upr2 chlamydomon
27	428.5	8.2	699	1	NIMA_EMENI	P11837 emericella
28	427	8.2	302	2	Q6IUI3	Q6iu13 xenopus lae
29	427	8.2	389	2	Q9W623	Q9w623 xenopus lae
30	425	8.2	443	2	Q91Z18	Q91z18 mus musculu
31	424	8.1	405	2	Q7QUR6	Q7qur6 giardia lam
32	423	8.1	445	1	NEK2_HUMAN	P51955 homo sapien
33	422.5	8.1	302	2	Q19530	Q19530 caenorhabdi
34	422	8.1	443	1	NEK2_MOUSE	O35942 mus musculu
35	417	8.0	893	2	Q659I9	Q659i9 sphaerechin
36	416	8.0	443	2	Q921N9	Q921n9 mus musculu
37	415	8.0	1090	2	Q9N9J2	Q9n9j2 leishmania
38	414.5	7.9	366	2	Q8BP64	Q8bp64 mus musculu
39	414.5	7.9	443	2	Q6PFG1	Q6pfg1 mus musculu
40	412	7.9	384	2	Q96QN9	Q96qn9 homo sapien
41	411	7.9	449	2	Q6BHW6	Q6bhw6 debaryomyce
42	410	7.9	1090	2	Q9GRT3	Q9grt3 leishmania
43	409	7.8	440	2	Q7ZUN2	Q7zun2 brachydanio
44	408.5	7.8	812	2	Q6UPR1	Q6upr1 chlamydomon
45	408	7.8	566	2	Q6BK92	Q6bk92 debaryomyce

ALIGNMENTS

RESULT 1
Q96MB3
ID Q96MB3 PRELIMINARY; PRT; 484 AA.
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ32685.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK057247; BAB71395.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; Pkinase; 1.

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DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Kinase.
SQ   SEQUENCE   484 AA;  54220 MW;  8FDE78BFA255BEB3 CRC64;

  Query Match             47.0%;  Score 2451;  DB 2;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-111;
  Matches  475;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        542 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 69

Qy        602 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 129

Qy        662 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 189

Qy        722 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 249

Qy        782 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 309

Qy        842 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 369

Qy        902 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 429

Qy        962 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 484


RESULT 2
Q6ZWH5
ID   Q6ZWH5      PRELIMINARY;      PRT;   712 AA.
AC   Q6ZWH5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein FLJ41066.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RA   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA   Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA   Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA   Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA   Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA   Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B.,
RA   Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK123061; BAC85527.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW   ATP-binding; Kinase; Transferase.
SQ   SEQUENCE   712 AA;  81623 MW;  58ECB713BC90B8A2 CRC64;

  Query Match             46.3%;  Score 2413;  DB 2;  Length 712;
  Best Local Similarity   84.2%;  Pred. No. 1.4e-109;
  Matches  490;  Conservative    9;  Mismatches   27;  Indels   56;  Gaps    4;

Qy         12 PTVYFKN------------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQ 59
              |:::|              |    | |||        : :  ||||||||||||||||
Db        128 PSIHFLRVLICLRLLMRDPCYQEILHSLGG--------IENLAQYMEIVANEYLGYGEEQ 179

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        180 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAES 239

Qy        119 ---------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                         ||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              |||||||||||||||||          |:     : : |   ||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVL 545
              |||||||||||||||||||||||||||||||||||||||||| : |
Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCVQHL 701


RESULT 3
Q86XB1
ID   Q86XB1      PRELIMINARY;      PRT;   474 AA.
AC   Q86XB1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   FLJ32685 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC045758; AAH45758.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004672; F:protein kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ   SEQUENCE   474 AA;  53074 MW;  D698CFEC2B43130F CRC64;

  Query Match            45.6%;  Score 2376;  DB 2;  Length 474;
  Best Local Similarity  97.9%;  Pred. No. 5.1e-108;
  Matches  465;  Conservative    0;  Mismatches    0;  Indels   10;  Gaps    1;

Qy        542 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 69

Qy        602 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 129

Qy        662 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 189

Qy        722 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 249

Qy        782 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 309

Qy        842 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 901
              ||||||          ||||||||||||||||||||||||||||||||||||||||||||||
Db        310 RNLKDH----------ASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 359

Qy        902 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 419

Qy        962 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 474
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RESULT 4
Q7Z671
ID   Q7Z671      PRELIMINARY;      PRT;   651 AA.
AC   Q7Z671;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp779L2259 (Fragment).
GN   Name=DKFZp779L2259;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX537852; CAD97860.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004672; F:protein kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW   ATP-binding; Hypothetical protein; Kinase; Transferase.
FT   NON_TER       1       1
SQ   SEQUENCE   651 AA;  74454 MW;  74717460AD34B2FA CRC64;

  Query Match            43.7%;  Score 2276;  DB 2;  Length 651;
  Best Local Similarity  83.5%;  Pred. No. 5.9e-103;
  Matches  462;  Conservative    9;  Mismatches   26;  Indels   56;  Gaps    4;

Qy         12 PTVYFKN------------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGBEQ 59
              |:::|              |    | |||         : :  ||||||||||||||||||
Db         54 PSIHFLRVLICLRLLMRDPCYQEILHSLGG--------IENLAQYMEIVANEYLGYGBEQ 105

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAEG 165

Qy        119 ----------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                         ||||||||||||||||||||||||||||||
Db        166 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 225

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 285

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 345

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              |||||||||||||||||          |:     : : |   ||||||||||||||||
Db        346 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 405

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        406 AYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKVRKH 465

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 525
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Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 585

Qy        504 NIMLGDKDKVTVT 516
              |||||||||||||:
Db        586 NIMLGDKDKVTVS 598


RESULT 5
Q8N774
ID   Q8N774      PRELIMINARY;      PRT;   404 AA.
AC   Q8N774;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ25966.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA   Arita M., Musashino K., Yuuki H., Hara H., Suzuki Y., Hata H.,
RA   Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA   Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA   Nagai K., Isogai T., Sugano S.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK098832; BAC05427.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004672; F:protein kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
SQ   SEQUENCE   404 AA;  45281 MW;  CAF5F519F843B88E CRC64;

  Query Match             39.5%;  Score 2057;  DB 2;  Length 404;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-92;
  Matches  401;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        448 MELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIML 507
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIML 60

Qy        508 GDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMA 567
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMA 120

Qy        568 TLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMI 627
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMI 180

Qy        628 SDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASL 687
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASL 240

Qy        688 SSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVD 747
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVD 300

Qy        748 DELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALLPLDL 807
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALLPLDL 360

Qy        808 LLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHG 848
              |||||||||||||||||||||||||||||||||||||||||
Db        361 LLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHG 401


RESULT 6
NEK1_CAEEL
ID   NEK1_CAEEL     STANDARD;      PRT;   959 AA.
AC   P84199;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Serine/threonine protein kinase D1044.8 (EC 2.7.1.37).
GN   ORFNames=D1044.8;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   REVISIONS.
RG   WormBase consortium;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- COFACTOR: Magnesium (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. NIMA
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U00065; AAK68286.2; -.
DR   WormBase; WBGene00017033; D1044.8.
DR   WormPep; D1044.8; CE32174.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Magnesium; Metal-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN      431    703       Protein kinase.
FT   NP_BIND     437    445       ATP (By similarity).
FT   BINDING     466    466       ATP (By similarity).
FT   ACT_SITE    569    569       Proton acceptor (By similarity).
SQ   SEQUENCE   959 AA;  109250 MW;  CABEA9C44BD534FC CRC64;

  Query Match             22.2%;  Score 1156;  DB 1;  Length 959;
  Best Local Similarity   30.4%;  Pred. No. 4.2e-48;
  Matches  312;  Conservative  184;  Mismatches  296;  Indels  236;  Gaps   31;

Qy         13 TVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH----TVDKLVNM 68
              |  ::||                          |  : :|: :|     :|    ||   :|:
Db        116 TKSYRNCK--------------------FQTFQFIASRFL---RSEHDWNVTVVNCLNV 151

Qy         69 TYIFQKLA-AVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE--------R 119
              |   |||    :: |::|  :     || ||  |   ||  ||  |  |::
Db        152 T---QKLIDNGENARKFVDCNLEDAVLV-LLATRQMTVLQHSLEILGRLSDWSTTCRENL 207
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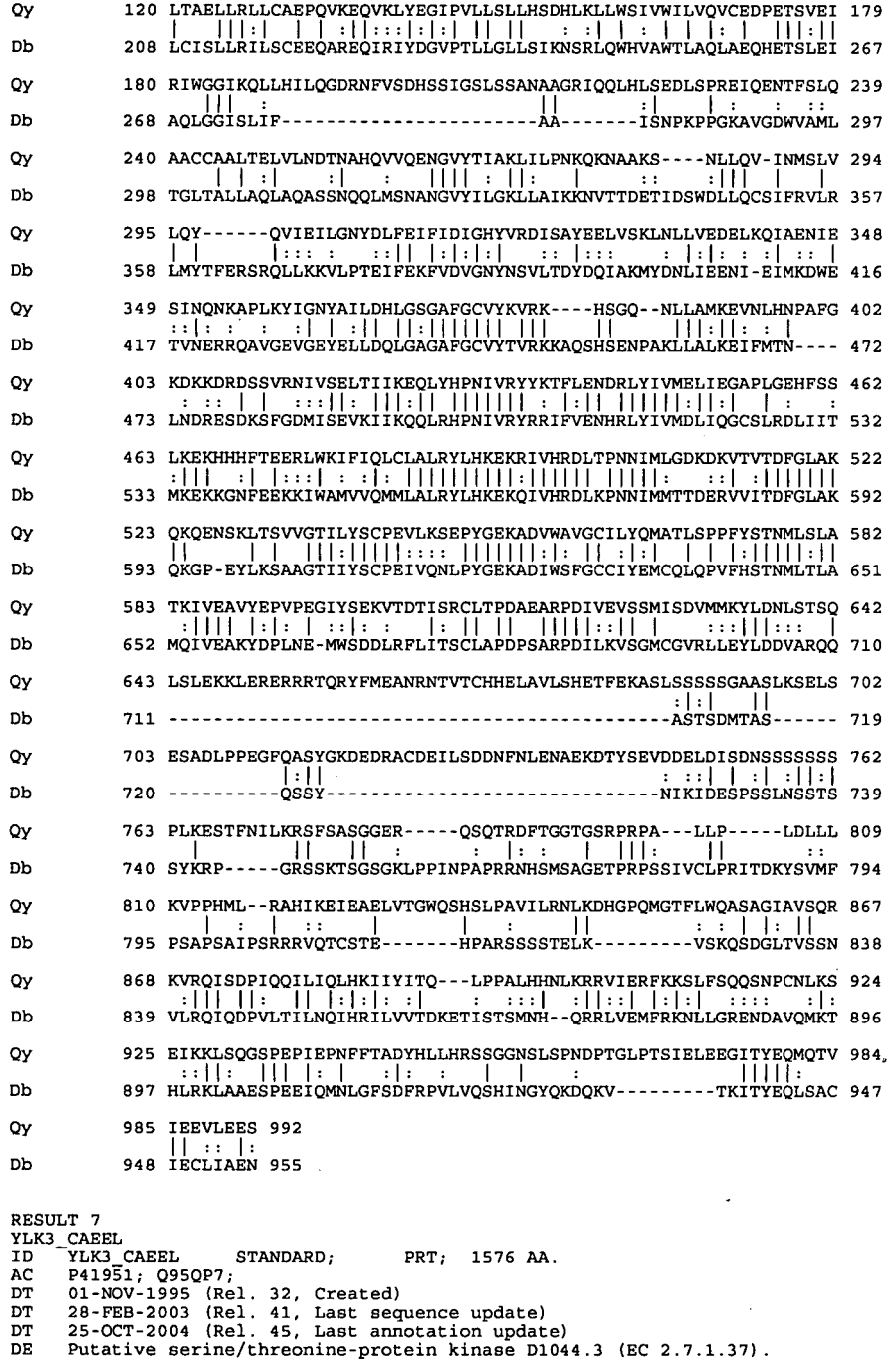

RESULT 7
YLK3_CAEEL
ID YLK3_CAEEL STANDARD; PRT; 1576 AA.
AC P41951; Q95QP7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative serine/threonine-protein kinase D1044.3 (EC 2.7.1.37).
GN ORFNames=D1044.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=a;
CC IsoId=P41951-1; Sequence=Displayed;
CC Name=b;
CC IsoId=P41951-2; Sequence=VSP_004900, VSP_004901;
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U00065; AAK68286.1; -.
DR EMBL; U00065; AAL27237.1; -.
DR HSSP; Q06486; 1CKI.
DR WormBase; WBGene00004114; D1044.3.
DR WormBase; WBGene00017033; D1044.8.
DR WormPep; D1044.3a; CE27894.
DR WormPep; D1044.3b; CE29743.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 8.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00289; WR1; 8.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; Hypothetical protein;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 431 703 Protein kinase.
FT NP_BIND 437 445 ATP (By similarity).
FT BINDING 461 461 ATP (By similarity).
FT ACT_SITE 569 569 Proton acceptor (By similarity).
FT VARSPLIC 1 904 Missing (in isoform b).
FT /FTId=VSP_004900.
FT VARSPLIC 905 1012 SPEEIQMNLGFSDFRPVLVQSHINGYQKDQKVTKITYEQLS
FT ACIECLIAENPAAKHVPHRTRAVVILRRDLLVLGQYVNMLV
FT PTITTYVVIRQIHVSLAAILVYTEYE -> MEETCSESPKE
FT SNIISFIWHKLLKRVPPPIMICLFFLLLQIFVISVVSQCPP
FT GLTPLFSNSNFNQPLTCTPQDACSCYSSSGSSRFGTICQYA
FT STYNNYICCYSTNTQ (in isoform b).
FT /FTId=VSP_004901.
SQ SEQUENCE 1576 AA; 174677 MW; 3A11EE573E813498 CRC64;

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  Query Match             22.2%;  Score 1156;  DB 1;  Length 1576;
  Best Local Similarity   30.4%;  Pred. No. 8.3e-48;
  Matches  312;  Conservative  184;  Mismatches  296;  Indels  236;  Gaps   31;

Qy          13 TVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH----TVDKLVNM 68
               |  ::||                          |  : :|: :|     :|    ||   :|:
Db         116 TKSYRNCK--------------------FQTFQFIASRFL---RSEHDWNVTVVNCLNV 151

Qy          69 TYIFQKLA-AVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE--------R 119
               |   |||    :: |::|  :      || ||  |   ||  ||   |  |::
Db         152 T---QKLIDNGENARKFVDCNLEDAVLV-LLATRQMTVLQHSLEILGRLSDWSTTCRENL 207

Qy         120 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEI 179
               |   |||:|  | | :||:::|:|:| || ||   : :| | : | | |: |  |||:||
Db         208 LCISLLRILSCEEQAREQIRIYDGVPTLLGLLSIKNSRLQWHVAWTLAQLAEQHETSLEI 267

Qy         180 RIWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQ 239
                  |||  :                          ||       :|    | :   :  ::
Db         268 AQLGGISLIF----------------------AA-------ISNPKPPGKAVGDWVAML 297

Qy         240 AACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKS----NLLQV-INMSLV 294
                 | | :|    :|   :   |||| : ||:   |     ::    :|||  |   |
Db         298 TGLTALLAQLAQASSNQQLMSNANGVYILGKLLAIKKNVTTDETIDSWDLLQCSIFRVLR 357

Qy         295 LQY------QVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIE 348
               | |       |::: :   ::|| |:|:|:|   :: |:::    : |:|: : :|  :: |
Db         358 LMYTFERSRQLLKKVLPTEIFEKFVDVGNYNSVLTDYDQIAKMYDNLIEENI-EIMKDWE 416

Qy         349 SINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRK----HSGQ--NLLAMKEVNLHNPAFG 402
               ::|: :  :  :| | :|| ||:|||||| |||     ||      |||:||: : |
Db         417 TVNERRQAVGEVGEYELLDQLGAGAFGCVYTVRKKAQSHSENPAKLLALKEIFMTN---- 472

Qy         403 KDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSS 462
                : :: | |  :::||: |||:|| |||||| : |:|| ||||||:||:|  | :   :
Db         473 LNDRESDKSFGDMISEVKIIKQQLRHPNIVRYRRIFVENHRLYIVMDLIQGCSLRDLIIT 532

Qy         463 LKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK 522
               :|||  :| |:::| : :|: ||||||||||:|||||| |||||:   ::| :|||||||
Db         533 MKEKKGNFEEKKIWAMVVQMMLALRYLHKEKQIVHRDLKPNNIMMTTDERVVITDFGLAK 592

Qy         523 QKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLA 582
               ||      | |  |||:|||||:::: |||||||:|: || :|:|  | | |:|||||:||
Db         593 QKGP-EYLKSAAGTIIYSCPEIVQNLPYGEKADIWSFGCCIYEMCQLQPVFHSTNMLTLA 651

Qy         583 TKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQ 642
                :|||| |:|: | ::|: :    |: || ||  |||||::|| |    :::|||:::  |
Db         652 MQIVEAKYDPLNE-MWSDDLRFLITSCLAPDPSARPDILKVSGMCGVRLLEYLDDVARQQ 710

Qy         643 LSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELS 702
                                                          :|:|   ||
Db         711 ------------------------------------------------ASTSDMTAS------ 719

Qy         703 ESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSS 762
                       |:||                                 : ::| | :| :||:|
Db         720 ----------QSSY----------------------------NIKIDESPSSLNSSTS 739

Qy         763 PLKESTFNILKRSFSASGGER-----QSQTRDFTGGTGSRPRPA---LLP-----LDLLL 809
                  |     ||   ||  :      :  |: :   |  |||:    ||       ::
Db         740 SYKRP-----GRSSKTSGSGKLPPINPAPRRNHSMSAGETPRPSSIVCLPRITDKYSVMF 794

Qy         810 KVPPHML--RAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQR 867
                  |  :  |  ::    |       |   :     ||          : : | |: ||
Db         795 PSAPSAIPSRRRVQTCSTE-------HPARSSSSTELK---------VSKQSDGLTVSSN 838

Qy         868 KVRQISDPIQQILIQLHKIIYITQ---LPPALHHNLKRRVIERFKKSLFSQQSNPCNLKS 924
                :||| ||:  || |:|:|: :|     :  :::|  :||::| |:|:|  ::::   :|:
Db         839 VLRQIQDPVLTILNQIHRILVVTDKETISTSMNH--QRRLVEMFRKNLLGRENDAVQMKT 896

Qy         925 EIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQTV 984
                ::||:  ||| |: |   :|:  :   |  |    :                |||||:
Db         897 HLRKLAAESPEEIQMNLGFSDFRPVLVQSHINGYQKDQKV---------TKITYEQLSAC 947

Qy         985 IEEVLEES 992
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               || :: |:
Db         948 IECLIAEN 955


RESULT 8
Q6DEH7
ID   Q6DEH7      PRELIMINARY;      PRT;   297 AA.
AC   Q6DEH7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Zgc:100962.
GN   Name=zgc:100962;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Singapore local strain; TISSUE=Embryo, and Whole;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RA   Director MGC Project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC077138; AAH77138.1; -.
DR   EMBL; BC081618; AAH81618.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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SQ   SEQUENCE   297 AA;  34233 MW;  DFE997C97F0F260E CRC64;

  Query Match             8.7%;  Score 456;  DB 2;  Length 297;
  Best Local Similarity   34.9%;  Pred. No. 1.2e-14;
  Matches   95;  Conservative   58;  Mismatches  103;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : |:||   :| | |  ||:         ::|:|:: : :    | ::|        : |:
Db         27 LANFAIEKKIGRGQFSEVYRATYVLDHTIVALKKIQIFDLMDAKARQD-------CIKEI 79

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| || |||:::|: :|:| : | ||:|| :   | :     |::      |: :|| |
Db         80 DLLK-QLNHPNVIKYHASFIEENELNIVLELADAGDLSQMIRHFKKQRRLIPEKTVWKYF 138

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
              :||| || ::|  :||:|||: | |: :     | : | ||   :  :|| |   |:|||
Db        139 VQLCSALEHMH-SRRIMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 195

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594
                |  || :    |  |:|:|::||:||:|| |  |||    |: ||  || :  | |:|
Db        196 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLP 255

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDIVEVSSM 626
                ||:::   :  |: || | ||||  | ||
Db        256 SDHYSQELRKLVDMCINPDPEKRPDITYVYSM 287


RESULT 9
Q7T001
ID   Q7T001      PRELIMINARY;      PRT;   284 AA.
AC   Q7T001;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   SI:zC167P9.4 (Novel protein similar to human NIMA (Never in mitosis
DE   gene a)-related kinase 7 (NEK7)) (Fragment).
GN   Name=SI:zC167P9.4;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clark G.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL772368; CAE30393.1; -.
DR   HSSP; P24941; 1OIQ.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT   NON_TER       1      1
SQ   SEQUENCE   284 AA;  32773 MW;  4A6BED4E4270810C CRC64;

  Query Match             8.7%;  Score 454;  DB 2;  Length 284;
  Best Local Similarity   36.1%;  Pred. No. 1.4e-14;
  Matches   96;  Conservative   52;  Mismatches  102;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : |: |   :| | |  ||:         :|:|:| :      | ::|        | |:
Db         13 LSNFLIEKKIGRGQFSEVYRATCLLNNQKVALKKVQIFEMMDAKARQD-------CVKEI 65

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| || |||:::|  :|: |: | ||:||      | :      |:|      |  :|| |
Db         66 DLLK-QLNHPNVIKYLDSFIANNELNIVLELASAGDLSQMIMHFKKKRRLIPERTIWKYF 124

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
              :||| || ::|  :|::|||: | |: :     :| : | ||   :  :|| |   |:|||
Db        125 VQLCSALEHMH-SRRVMHRDIKPANVFITASGEVKLGDLGLG--RFFSSKTTAAHSLVGT 181

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYS--TNMLSLATKIVEAVYEPVP 594
                |  || :    |  |:|:|::||:||:|| |  ||||    |:|||  || :  | |:|
Db        182 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALHSPFYSDKMNLLSLCHKIEQCEYPPLP 241

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDI 620
                ||:|  | :| |: |: : ||||
Db        242 TEHYSQKFRDLVSMCINPEPDQRPDI 267


RESULT 10
Q6BVX7
ID   Q6BVX7      PRELIMINARY;      PRT;   580 AA.
AC   Q6BVX7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Similar to sp|P22209 Saccharomyces cerevisiae YAR018c KIN3 ser/thr
DE   protein kinase.
GN   ORFNames=DEHA0B16071g;
OS   Debaryomyces hansenii CBS767.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX   NCBI_TaxID=284592;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS767;
RG   Genolevures;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA   Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA   Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA   Wincker P., Souciet J.L.;
RT   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS767;
RA   Genoscope;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; CR382134; CAG85656.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
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DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   580 AA;  68140 MW;  94DDB5AF3A0D2406 CRC64;

  Query Match             8.6%;  Score 450.5;  DB 2;  Length 580;
  Best Local Similarity   23.0%;  Pred. No. 5.4e-14;
  Matches  159;  Conservative  106;  Mismatches  232;  Indels  193;  Gaps   24;

Qy        363 YAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTII 422
              |  |: :| |::| | ||:: |   :   ||:  ::     : ::|:     ::||| |:
Db         10 YDALEVIGKGSYGTVRKVQEKSSGEIFVRKEIEYNS----MNNQERN----QLISELRIL 61

Qy        423 KEQLYHPNIVRYYK--TFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFI 480
              :| | |||||:|::    ::   ::| ||  :|  | :  |: ::      || :|:: :
Db         62 RE-LNHPNIVKYFRHDHIMQKKSIHIYMEYCDGGDLAQVISNFRKNKEMVPEEFIWQVLV 120

Qy        481 QLCLALRYLH----------------------KEKRIVHRDLTPNNI-MLGDKDKVTVT 516
              |  |||   |                     |  ::|||: |:|| ||     : :
Db        121 QTLLALHRCHYGIDAKKVNLFSNPVDDKEPTIDSETVVIHRDIKPDNIFMLNSGKSIKLG 180

Qy        517 DFGLAKQ-KQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYS 575
              ||||||    :|    : |||  |  ||||   ||    |:|::||:|::: || ||| :
Db        181 DFGLAKMLTSQNDFAKTYVGTPYYMSPEVLMDNPYSPVCDIWSLGCVLFELCTLQPPFQA 240

Qy        576 TNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYL 635
              | | :|| : :   :| |||| ::   |  |:| | | ||   ::          |
Db        241 KTHLQLQSKIKQGIIPDLP-GIYSSQLRSIIKECITVDPELRPSCYDL----------L 288

Qy        636 DNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAA 695
              : ||   |  | :|:           | | |     :|   : |  :| ||
Db        289 ETLSIRFLRKEMELK----------EINTNLNEFQKQLLTKNDELKKKESL-------- 329

Qy        696 SLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDD---ELDI 752
                                                  | | |:  ::: :|   | :
Db        330 -------------------------------------LNNIERKIFAQREDLENEYNN 350

Qy        753 SDNSSSSSSSPLKE---STFNILKRSFSASGGE-RQSQTRDFTGGTGSRPRPALLPLDLL 808
                :|    |:|     | : |:|      | |    |:|
Db        351 MQKKCNSQKKQLEEELIEEFEMRKKSMDQEAKEVRLGYQREFK---------------- 393

Qy        809 LKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRK 868
              |  | ::  :|:|     | | |                              |::
Db        394 -MVVEHEVQLRLKDI-----LGKQKH------------------------------QQQ 416

Qy        869 VRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLKSEIKK 928
              :|     ||  :| |:           | :  :    ::      || |     |  |
Db        417 QQQ-----QQQHLQQHQ---------QQHQHQNQHQHPQY------QQPQPYQELSRKKS 456

Qy        929 LSQGSPEPIEPNFFTADYHLLHRSS-GGNSLSPNDPTGLPTSIELEE--GITYEQMQTVI 985
                || | :       |   | ::   : : || | | |  ::|::   :   |:   |
Db        457 DPLSSPSPSKATTRNTLYLANHYAAPNEHVVLPNKPKG-PKELQLDDQSKLLSPQLTRRI 515

Qy        986 EEVLEESGYYNFTSNRYHSYPWGTKNHPTK 1015
                  |   :: || |:|  :  |: ||:
Db        516 PLKTRNSENSDYDSNGYYSDQY--KSSPTR 543


RESULT 11
NEK6_MOUSE
ID   NEK6_MOUSE     STANDARD;      PRT;   313 AA.
AC   Q9ES70; Q8C6E6; Q9D0E2; Q9DBI8;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Serine/threonine-protein kinase Nek6 (EC 2.7.1.37) (NimA-related
DE   protein kinase 6).
GN   Name=Nek6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RX   MEDLINE=20422672; PubMed=10964517; DOI=10.1006/geno.2000.6293;
RA   Kandli M., Feige E., Chen A., Kilfin G., Motro B.;
RT   "Isolation and characterization of two evolutionarily conserved murine
RT   kinases (Nek6 and Nek7) related to the fungal mitotic regulator,
RT   NIMA.";
RL   Genomics 68:187-196(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c, and C57BL/6J; TISSUE=Head, Liver, and Stomach;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- COFACTOR: Magnesium.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. NIMA
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF218847; AAG16653.1; -.
DR   EMBL; AK004925; BAB23676.2; -.
DR   EMBL; AK011519; BAB27673.2; -.
DR   EMBL; AK075717; BAC35907.1; -.
DR   EMBL; AK075836; BAC35995.1; -.
DR   EMBL; AK086700; BAC39721.1; -.
DR   EMBL; AK089919; BAC40995.1; -.
DR   EMBL; BC019524; AAH19524.1; -.
DR   HSSP; P24941; 1E1X.
DR   MGD; MGI:1891638; Nek6.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Magnesium; Metal-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       45    310       Protein kinase.
FT   NP_BIND      51     59       ATP (By similarity).
FT   BINDING      74     74       ATP (By similarity).
FT   ACT_SITE    172    172       Proton acceptor (By similarity).
FT   CONFLICT    210    210       T -> A (in Ref. 2; BAC35995).
FT   CONFLICT    244    244       Q -> R (in Ref. 2; BAB23676).
FT   CONFLICT    246    246       P -> R (in Ref. 2; BAC35995).
SQ   SEQUENCE   313 AA;  35742 MW;  14A8BC9F2C34397C CRC64;

  Query Match             8.5%;  Score 445;  DB 1;  Length 313;
  Best Local Similarity   35.2%;  Pred. No. 4.3e-14;
  Matches   94;  Conservative   55;  Mismatches  106;  Indels   12;  Gaps    5;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : :: |   :| | |  |||      :  :|:|:| :      | ::|        | |:
Db         42 LADFQIEKKIGRGQFSEVYKATCLLDRKTVALKKVQIFEMMDAKARQD-------CVKEI 94

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
              ::| || ||||::|  :|:|:: | ||:|| :   | :     |::     |  :|| |
Db         95 GLLK-QLNHPNIIKYLDSFIEDNELNIVLELADAGDLSQMIKYFKKQKRLIPERTVWKYF 153

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAK-QKQENSKLTSVVGTIL 538
              :||| |: ::|  :|::|||: | |: :     | : | || :    | :   |:|||
Db        154 VQLCSAVEHMH-SRRVMHRDIKPANVFITATGIVKLGDLGLGRFFSSETTAAHSLVGTPY 212

Qy        539 YSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVPEG 596
              |  || :    |  |:|:|::||:||:|| |  |||     |: ||  || :  | |:|
Db        213 YMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLFSLCQKIEQCDYPPLPGE 272

Qy        597 IYSEKVTDTISRCLTPDAEARPDIVEV 623
              ||||: : :| |: || : ||||| |
Db        273 HYSEKLRELVSMCIYPDPDHRPDIVYV 299


RESULT 12
Q6DII1
ID   Q6DII1      PRELIMINARY;      PRT;   442 AA.
AC   Q6DII1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC075559; AAH75559.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   442 AA;  51976 MW;  33B5E1A0FF418CC5 CRC64;

  Query Match             8.5%;  Score 444.5;  DB 2;  Length 442;
  Best Local Similarity   28.3%;  Pred. No. 7.3e-14;
  Matches  132;  Conservative   86;  Mismatches  185;  Indels   63;  Gaps   15;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : :| :|  :|||::|   |:|: |   ||  ||::             ::  : :|||:
Db          5 VEDYEVLYTIGSGSYGKCQKIRRRSDGKLLVWKELDYGTMT--------EAEKQMLVSEV 56

Qy        420 TIIKEQLYHPNIVRYYKTFLE--NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWK 477
              :::| | ||||||||   ::  |  ||||||  ||  |    :  ::  :  |: : :
Db         57 NLLRE-LKHPNIVRYYDRIIDRTNTTLYIVMEYCEGGDLASLIAKCTKERQYLEEDFILR 115

Qy        478 IFIQLCLALRYLHKEK----RIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT-S 532
              || || |||:  ||       ::|||| | || |  |: | : |||||:    :|    :
Db        116 IFSQLALALKDCHKRSDGGHTVLHRDLKPANIFLDAKNNVKLGDFGLARILHHDSSFAKT 175

Qy        533 VVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEP 592
              ||| |  || :   | ||:|:|::||:||::  ||||| : |   || || |  :
Db        176 FVGTPYYMSPEQMNRMSYNEKSDIWSLGCLLYELCALSPPFTAYNQKELAEKIREGRFRR 235
```

```
Qy        593 VPEGIYSEKVTDTISRCLTPDAEARPDIVEV--SSMISDVM--------MKYLDNLSTSQ 642
              :|   |||::   |:  |       || | |:    ::::::          | |      :
Db        236 IPYR-YSEELNQVITNMLHLKDYLRPSIEEILQHHLLAELVREEQKKTEKKVLRAAEQER 294

Qy        643 LSL------EKKLERERRRT-QRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAA 695
              ||:      | :|: ::  | :|   |           || |      :| : : :
Db        295 LSMPDPVPSELRLKEQQLHTRERALREREERLEQRERELCVRERMAEDKLARAET----- 349

Qy        696 SLKSELSESADLPPEG--FQASYGKDEDRACDEILSDDNFNL-------ENAEKDTYSEV 746
              | :| :|  |   |||:   :|   |   :    ::       ||:  | | |
Db        350 -----LVKSFNLMKEQHLFQAALENGKDAYVDSSSTRSRRHVHFGSNSKENSSTDRYREQ 404

Qy        747 DDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTG 792
              :    ||      :: ::    : |:|::       | ::|   |
Db        405 E---KCSDLQKRLQAANIRAKALSELERNY-------QLKSRQILG 440
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RESULT 13
Q6DIX9
ID Q6DIX9 PRELIMINARY; PRT; 310 AA.
AC Q6DIX9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Nek7-prov protein.
GN Name=nek7-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC075406; AAH75406.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 310 AA; 36097 MW; 715E760614AD00BC CRC64;

Query Match 8.5%; Score 444; DB 2; Length 310;
Best Local Similarity 35.0%; Pred. No. 4.8e-14;
Matches 93; Conservative 57; Mismatches 100; Indels 16; Gaps 6;

```
Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
              : :: |   :| | |  ||:   |  :  :|:|:| :      | ::|        : |:
Db         39 LADFKIEKKIGRGQFSEVYRATCHLDRKPVALKKVQIFEMMDAKARQD-------CIKEI 91

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
               ::| || |||:::|  :|:|:: | ||:|| :   | :     |::     |  :|| |
Db         92 DLLK-QLNHPNVIKYLDSFIEDNELNIVLELADAGDLSQMIKYFKKQKRLIPERTVWKYF 150

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
              :||| |: ::|  :||:|||: | |: :     | : | ||   :  :|| |   |:|||
Db        151 VQLCSAVEHMH-SRRIMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 207

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNM--LSLATKIVEAVYEPVP 594
                | || :   |  |:|:|::||:||:|| |  |||   |   ||  || :  | |:|
Db        208 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMSLFSLCQKIEQCDYPPLP 267

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDI 620
              :  ||||: : :| |: || : ||||
Db        268 KEHYSEKLRELVSMCIYPDPDQRPDI 293
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RESULT 14
Q8T755
ID Q8T755 PRELIMINARY; PRT; 299 AA.
AC Q8T755;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21980198; PubMed=11967531; DOI=10.1038/ng855;
RA Abi-Rached L., Gilles A., Shiina T., Pontarotti P., Inoko H.;
RT "Evidence of en bloc duplication in vertebrate genomes.";
RL Nat. Genet. 31:100-105(2002).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF391294; AAM18889.1; -.
DR HSSP; P24941; 1E1X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.

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SQ   SEQUENCE   299 AA;  34507 MW;  BEFB9E58F3A1D689 CRC64;

  Query Match             8.5%;  Score 443;  DB 2;  Length 299;
  Best Local Similarity   34.1%;  Pred. No. 5.1e-14;
  Matches   92;  Conservative   57;  Mismatches  105;  Indels   16;  Gaps    6;

Qy        356 PLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNI 415
Db         19 PYNTLRNFTIEKKIGRGQFSVVYRAQNLVNGKDVALKKVQIFEMMDAKARQD-------C 71

Qy        416 VSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERL 475
Db         72 IKEIDLLK-QLNHPNVIQYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTI 130

Qy        476 WKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---S 532
Db        131 WKYFVQLCSALEHMH-SRRVMHRDIKPANVFITATGVVKLGDLGLG--RFFSSKTTAAHS 187

Qy        533 VVGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVY 590
Db        188 LVGTPYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDY 247

Qy        591 EPVPEGIYSEKVTDTISRCLTPDAEARPDI 620
Db        248 PPLPSEHYSDELRHLVNICINPDPDKRPDI 277


RESULT 15
Q7ZSX4
ID   Q7ZSX4      PRELIMINARY;      PRT;   310 AA.
AC   Q7ZSX4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Nek6-prov protein (NIMA-family kinase Nek6).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Roig J., Avruch J.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC044326; AAH44326.1; -.
DR   EMBL; AY271413; AAP31901.1; -.
DR   HSSP; P24941; 1OIQ.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   310 AA;  36053 MW;  F94DAD81464F8FC4 CRC64;

  Query Match             8.5%;  Score 442;  DB 2;  Length 310;
  Best Local Similarity   34.6%;  Pred. No. 6e-14;
  Matches   92;  Conservative   58;  Mismatches  100;  Indels   16;  Gaps    6;

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419
Db         39 LADFKIEKKIGRGQFSEVYKATCHLDRKPVALKKVQIFEMMDAKARQD-------CIKEI 91

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
Db         92 DLLK-QLNHPNVIKYLDSFIEDNELNIVLEIADAGDLSQMIKYFKKQKRLIPERTVWKYF 150

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLT---SVVGT 536
Db        151 VQLCSAVEHMH-SRRIMHRDIKPANMFITATGVVKLGDLGLG--RFFSSKTTAAHSLVGT 207

Qy        537 ILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFY--STNMLSLATKIVEAVYEPVP 594
Db        208 PYYMSPERIHENGYNFKSDIWSLGCLLYEMAALQSPFYGDKMNLFSLCQKIEQCDYPPLP 267

Qy        595 EGIYSEKVTDTISRCLTPDAEARPDI 620
Db        268 KEHYSEKLRELVGMCIYPDPDQRPDI 293


Search completed: May 10, 2005, 14:47:30
Job time : 187 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 14:29:14 ; Search time 169 Seconds
(without alignments)
2325.139 Million cell updates/sec

Title: PCT-US03-32302-2
Perfect score: 5214
Sequence: 1 MRVLFDESVLPPTVYFKNCS.....FTSNRYHSYPWGTKNHPTKR 1016

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5214	100.0	1016	8	ADN36594	Adn36594 Human pro
2	4587.5	88.0	1125	8	ADJ96636	Adj96636 Human Nim
3	4516.5	86.6	1115	7	AAE39514	Aae39514 Human 148
4	4516.5	86.6	1115	8	ADQ15170	Adq15170 Human can
5	4149	79.6	854	4	AAG67391	Aag67391 Partial a
6	4149	79.6	854	7	AAE39519	Aae39519 Human SGK
7	4149	79.6	854	8	ADN36596	Adn36596 Human pro
8	2451	47.0	484	6	ADA55439	Ada55439 Human pro
9	2413	46.3	712	8	ADQ67014	Adq67014 Novel hum
10	1172	22.5	229	4	AAU17282	Aau17282 Novel sig
11	1172	22.5	229	7	ADB93990	Adb93990 Human nov
12	1129	21.7	223	4	AAU87169	Aau87169 Novel cen
13	1129	21.7	223	8	ADI54484	Adi54484 Novel hum
14	980.5	18.8	261	5	AAU96909	Aau96909 Human ser
15	520	10.0	106	4	AAU17603	Aau17603 Novel sig
16	520	10.0	106	4	AAM95881	Aam95881 Human rep
17	520	10.0	106	4	ABB96412	Abb96412 Human tes
18	520	10.0	106	4	AAU87485	Aau87485 Novel cen
19	520	10.0	106	7	ADB94311	Adb94311 Human nov
20	520	10.0	106	8	ADI54800	Adi54800 Novel hum
21	440	8.4	306	5	AAU97064	Aau97064 Serine/th
22	440	8.4	306	7	ADD89981	Add89981 Human can
23	440	8.4	306	8	ADO55903	Ado55903 Human NIM
24	440	8.4	313	5	ABP61443	Abp61443 Human NF-
25	440	8.4	313	8	ADH16907	Adh16907 Human Nek
26	440	8.4	313	8	ADO55902	Ado55902 Human NIM
27	440	8.4	330	4	AAU87410	Aau87410 Novel cen
28	440	8.4	330	8	ADI54725	Adi54725 Novel hum
29	438	8.4	302	3	AAY59143	Aay59143 Human ser
30	438	8.4	302	3	AAY84320	Aay84320 Human car
31	438	8.4	302	4	AAB71956	Aab71956 Human TGF
32	438	8.4	302	8	ADH16909	Adh16909 Human Nek
33	438	8.4	311	4	AAG75475	Aag75475 Human col
34	436	8.4	268	3	AAY59146	Aay59146 Human ser
35	435	8.3	302	4	AAB50054	Aab50054 Murine De
36	434.5	8.3	735	4	ABB66233	Abb66233 Drosophil
37	434	8.3	499	5	ABJ05583	Abj05583 Breast ca
38	433	8.3	313	3	AAB22799	Aab22799 Human nek
39	433	8.3	369	3	AAY59145	Aay59145 Human ser
40	423	8.1	445	3	AAY92330	Aay92330 Human NlK
41	423	8.1	445	6	ABR58566	Abr58566 Human can
42	423	8.1	445	6	ABR48219	Abr48219 Human bla
43	423	8.1	445	6	ABP71714	Abp71714 NEK-like
44	423	8.1	445	6	ABP97692	Abp97692 Amino aci
45	423	8.1	445	7	ADB80466	Adb80466 Ovarian c

ALIGNMENTS

RESULT 1
ADN36594
ID ADN36594 standard; peptide; 1016 AA.
XX
AC ADN36594;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human protein kinase HPK3P23 protein sequence.
XX
KW cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischemia; reperfusion.
XX
OS Homo sapiens.
XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
DR N-PSDB; ADN36593.
XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Claim 8; SEQ ID NO 2; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,

```
CC   preventing and treating kinase-related diseases, in particular, diseases
CC   associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC   Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC   osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC   autoimmune disorders, retinal detachment, stroke, epilepsy or
CC   ischemia/reperfusion. This sequence corresponds to the HPK3P23 protein.
XX
SQ   Sequence 1016 AA;

  Query Match            100.0%;  Score 5214;  DB 8;  Length 1016;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1016;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60

Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180

Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQVINMSLVLQYQVI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQVINMSLVLQYQVI 300

Qy        301 EILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYI 360

Qy        361 GNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELT 420

Qy        421 IIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFI 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFI 480

Qy        481 QLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540

Qy        541 CPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSE 600

Qy        601 KVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYF 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 KVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYF 660

Qy        661 MEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDE 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 MEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDE 720

Qy        721 DRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASG 780

Qy        781 GERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVI 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVI 840

Qy        841 LRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNL 900

Qy        901 KRRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSP 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 KRRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSP 960

Qy        961 NDPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NDPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016


RESULT 2
ADJ96636
ID   ADJ96636 standard; protein; 1125 AA.
XX
AC   ADJ96636;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human Nim-A related protein kinase NEK10 protein SeqID 93.
XX
KW   kinase; human; SNP; single nucleotide polymorphism;
KW   tyrosine protein kinase; serine/threonine protein kinase; PTK; STK;
KW   gene therapy; cancer; immune-related disease; cardiovascular disease;
KW   brain; neuronal associated disease; metabolic; inflammatory disorder;
KW   cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme;
KW   Nim-A related protein kinase; NEK10.
XX
OS   Homo sapiens.
OS   57.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 325
FT                   /note= "Wild type Ser substituted for Thr by single
FT                   nucleotide polymorphism"
FT   Misc-difference 931
FT                   /note= "Wild type Ser substituted for Asn by single
FT                   nucleotide polymorphism"
XX
PN   WO2004006838-A2.
XX
PD   22-JAN-2004.
XX
PF   15-JUL-2003; 2003WO-US021730.
XX
PR   15-JUL-2002; 2002US-0395632P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Whyte D,  Manning G,  Caenepeel S;
XX
DR   WPI; 2004-122753/12.
DR   N-PSDB; ADJ96570.
XX
PT   New nucleic acid molecule encoding a kinase polypeptide, useful for
PT   preparing a composition for treating diseases or disorders, e.g., cancer,
PT   or neurological, immunological or inflammatory disorders.
XX
PS   Claim 1; SEQ ID NO 93; 366pp; English.
XX
CC   This invention relates to a novel isolated, enriched or purified nucleic
CC   acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC   to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC   as well as protein kinase-like enzymes. The present invention describes
CC   screening methods to identify agonists, antagonists and antibodies that
CC   can be used to modulate the activity or function of the mammalian kinase
CC   enzymes. As such, these compositions can be used for gene therapy
CC   purposes to treat diseases or disorders including cancer, immune-related
CC   diseases, cardiovascular disease, brain or neuronal associated disease,
CC   metabolic and inflammatory disorders. Accordingly, they exhibit
CC   cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC   activities. This polypeptide sequence is a human kinase protein sequence
CC   of the invention.
XX
SQ   Sequence 1125 AA;
```

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  Query Match             88.0%;  Score 4587.5;  DB 8;  Length 1125;
  Best Local Similarity   87.1%;  Pred. No. 0;
  Matches  917;  Conservative    8;  Mismatches   25;  Indels  103;  Gaps    5;

Qy         12 PTVYFKN------------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQ 59
              |:::|              |    | |||         : :  ||||||||||||||||
Db        128 PSIHFLRVLICLRLLMRDPCYQEILHSLGG---------IENLAQYMEIVANEYLGYGEEQ 179

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        180 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAES 239

Qy        119 ---------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                          ||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              |||||||||||||||||        |:     : : |  ||||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 719

Qy        564 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 779

Qy        624 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 839

Qy        684 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 899

Qy        744 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALL 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRP--- 956

Qy        804 PLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIA 863
                                                ||||||||||||||||
Db        957 ------------------------------------------GPQMGTFLWQASAGIA 972

Qy        864 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 1032

Qy        924 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 1092

Qy        984 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              |||||||||||||||||||||||||||||||||
Db       1093 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1125
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RESULT 3
AAE39514
ID   AAE39514 standard; protein; 1115 AA.
XX
AC   AAE39514;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human 14815 protein.
XX
KW   Human; 14815 protein; therapy; neurological disease; apoptotic disease;
KW   metabolic disease; inflammatory disease; neuroprotective; cytostatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          198. .238
FT                   /note= "Armadillo/beta-catenin-like repeat domain"
FT   Domain          239. .279
FT                   /note= "Armadillo/beta-catenin-like repeat domain"
FT   Domain          280. .320
FT                   /note= "Armadillo/beta-catenin-like repeat domain"
FT   Domain          401. .448
FT                   /note= "Armadillo/beta-catenin-like repeat domain"
FT   Region          472. .500
FT                   /note= "Coiled coil structure"
FT   Domain          519. .779
FT                   /note= "Protein kinase domain"
XX
PN   US2003134317-A1.
XX
PD   17-JUL-2003.
XX
PF   02-JAN-2003; 2003US-00335711.
XX
PR   02-JAN-2002; 2002US-0345853P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers RE;
XX
DR   WPI; 2003-688693/65.
DR   N-PSDB; AAD59965.
XX
PT   New nucleic acid molecules, designated 14815 nucleic acids, useful for
PT   preparing a composition for diagnosing or treating neurological,
PT   inflammatory, apoptotic or metabolic diseases.
XX
PS   Claim 7; Page 44-46; 59pp; English.
XX
CC   The invention relates to novel 14815 protein, a member of kinase family
CC   and polynucleotide encoding such protein. Sequences of the invention are
CC   useful for detecting a molecule that binds to the polypeptide, including
CC   molecules that modulate their activity. They are useful in the diagnosis
CC   or treatment of neurological, inflammatory, apoptotic or metabolic
CC   diseases. The present sequence is human 14815 protein
XX
SQ   Sequence 1115 AA;

  Query Match             86.6%;  Score 4516.5;  DB 7;  Length 1115;
  Best Local Similarity   86.0%;  Pred. No. 0;
  Matches  906;  Conservative    8;  Mismatches   26;  Indels  113;  Gaps    5;

Qy         12 PTVYFKN------------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQ 59
              |:::|              |    | |||         : :  ||||||||||||||||
Db        128 PSIHFLRVLICLRLLMRDPCYQEILHSLGG---------IENLAQYMEIVANEYLGYGEEQ 179

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAES 239

Qy        119 ----------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                           ||||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
                ||||||||||||||||          |:     : : |   ||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 563
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 719

Qy        564 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 623
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 779

Qy        624 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 683
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 839

Qy        684 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 743
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 899

Qy        744 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALL 803
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRP--- 956

Qy        804 PLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIA 863
                                                                ||||||
Db        957 ------------------------------------------------------ASAGIA 962

Qy        864 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 923
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 1022

Qy        924 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 983
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 1082

Qy        984 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
                ||||||||||||||||||||||||||||||||
Db       1083 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1115


RESULT 4
ADQ15170
ID   ADQ15170 standard; protein; 1115 AA.
XX
AC   ADQ15170;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human cancer related polypeptide, 14815.
XX
KW   Cancer; angiogenic disorder; cytostatic; antiangiogenic; gene therapy;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2004058153-A2.
XX
PD   15-JUL-2004.
XX
PF   16-DEC-2003; 2003WO-US040226.
XX
PR   20-DEC-2002; 2002US-0435108P.
PR   23-DEC-2002; 2002US-0436443P.
PR   07-JAN-2003; 2003US-0438498P.
PR   31-JAN-2003; 2003US-0444370P.
PR   06-FEB-2003; 2003US-0446031P.
PR   11-MAR-2003; 2003US-0453635P.
PR   25-MAR-2003; 2003US-0457199P.
PR   10-APR-2003; 2003US-0462458P.
PR   30-APR-2003; 2003US-0466732P.
PR   08-MAY-2003; 2003US-0469184P.
PR   19-MAY-2003; 2003US-0471663P.
PR   03-JUN-2003; 2003US-0475472P.
PR   12-JUN-2003; 2003US-0478150P.
PR   23-JUN-2003; 2003US-0480631P.
PR   15-JUL-2003; 2003US-0487369P.
PR   29-JUL-2003; 2003US-0490866P.
PR   02-SEP-2003; 2003US-0499614P.
PR   09-OCT-2003; 2003US-0510081P.
PR   06-NOV-2003; 2003US-0517742P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lightcap ES,  Ecsedy JA,  Hunter JJ,  Macbeth KJ,  Nestor MT;
XX
DR   WPI; 2004-525772/50.
DR   N-PSDB; ADQ15169.
XX
PT   Identifying a compound capable of treating cancer or an angiogenic
PT   disorder by combining a compound to be tested with e.g., 15986, 2179 or
PT   13249 polypeptide and detecting binding of the test compound to the
PT   polypeptide.
XX
PS   Claim 1; SEQ ID NO 128; 576pp; English.
XX
CC   The invention relates to a novel method for identifying a compound
CC   capable of treating cancer or an angiogenic disorder. The method
CC   comprises: combining a compound to be tested with a cancer related
CC   polypeptide; and detecting binding of the test compound to the
CC   polypeptide. The invention further comprises: identifying a subject
CC   having or at risk for developing cancer; and treating a subject having a
CC   cancer or a cancer characterised by aberrant 15986, 2188, 20743, 9148,
CC   9151, 9791,44252, 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411,
CC   15088, 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694, 15701,
CC   53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201, 6985, 9883, 12238,
CC   18057, 21617, 39228, 49928, 54476, 62113, 64316, 12264, 32362, 58198,
CC   2887, 3205, 8557, 9600, 9693, 44867, 53058, 55556, 57658, 2208, 10252,
CC   10302, 14218, 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827,
CC   21708, 3801, 64698, 2179 or 13249 cancer related polypeptide activity or
CC   nucleic acid expression. The method and compounds have cytostatic and
CC   antiangiogenic activities. The cancer related genes may be used in gene
CC   therapy to treat disorders. The method is useful in identifying a
CC   compound capable of treating cancer or an angiogenic disorder. This
CC   sequence represents a human cancer related polypeptide used in the method
CC   of the invention.
XX
SQ   Sequence 1115 AA;
```

```
  Query Match           86.6%;  Score 4516.5;  DB 8;  Length 1115;
  Best Local Similarity  86.0%;  Pred. No. 0;
  Matches  906;  Conservative    8;  Mismatches   26;  Indels  113;  Gaps    5;

Qy         12 PTVYFKN------------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQ 59
              |:::|            |   | |||        : :  ||||||||||||||||||
Db        128 PSIHFLRVLICLRLLMRDPCYQEILHSLGG--------IENLAQYMEIVANEYLGYGEEQ 179

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAES 239

Qy        119 ----------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                           ||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              |||||||||||||||||          |:     : : |   ||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVLKSEPYGEKADVWAVGCIL 719

Qy        564 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 YQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEKVTDTISRCLTPDAEARPDIVEV 779

Qy        624 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 SSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFMEANRNTVTCHHELAVLSHETFE 839

Qy        684 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 KASLSSSSSGAASLKSELSESADLPPEGFQASYGKDEDRACDEILSDDNFNLENAEKDTY 899

Qy        744 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRPALL 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 SEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGGERQSQTRDFTGGTGSRPRP--- 956

Qy        804 PLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVILRNLKDHGPQMGTFLWQASAGIA 863
                                                                  ||||||
Db        957 ------------------------------------------------------ASAGIA 962

Qy        864 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 VSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLKRRVIERFKKSLFSQQSNPCNLK 1022

Qy        924 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 SEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPNDPTGLPTSIELEEGITYEQMQT 1082

Qy        984 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
                                 ||||||||||||||||||||||||||||||||
Db       1083 VIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1115
```

```
RESULT 5
AAG67391
ID   AAG67391 standard; protein; 854 AA.
XX
AC   AAG67391;
XX
DT   13-NOV-2001  (first entry)
XX
DE   Partial amino acid sequence of human protein kinase SGK237.
XX
KW   Human; protein kinase; cancer; immune disease; cardiovascular disease;
KW   brain disease; neuronal disease; Alzheimer's disease; chromosome 3;
KW   Parkinson's disease; multiple sclerosis; metabolic disorder;
KW   peripheral nervous system disease; amyotrophic lateral sclerosis;
KW   infection; ocular disease; migraine; pain; sexual dysfunction;
KW   mood disorder; attention disorder; cognition disorder; hypotension;
KW   hypertension; psychotic disorder; dyskinesia; transplant rejection.
XX
OS   Homo sapiens.
XX
PN   WO200166594-A2.
XX
PD   13-SEP-2001.
XX
PF   02-MAR-2001; 2001WO-US006838.
XX
PR   06-MAR-2000; 2000US-0187150P.
PR   29-MAR-2000; 2000US-0193404P.
PR   13-NOV-2000; 2000US-0247013P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX
DR   WPI; 2001-536777/59.
DR   N-PSDB; AAH77990.
XX
PT   Nucleic acids capable of encoding human polypeptides having a kinase or
PT   kinase-like activity, useful for diagnosing a disease selected from
PT   cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT   Alzheimer's disease).
XX
PS   Claim 7; Fig 2A; 201pp; English.
XX
CC   The present sequence represents a partial human protein kinase. The gene
CC   is located at chromosomal position 3p24.2-p21.3. The kinase polypeptides
CC   are useful for diagnosing a disease or disorder selected from cancers
CC   (e.g. cancers of tissues and cancers of hematopoietic origin), immune-
CC   related diseases and disorders, cardiovascular disease, brain or neuronal
CC   -associated diseases (e.g. Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis), metabolic disorders, peripheral nervous system
CC   diseases, amyotrophic lateral sclerosis, viral infections, infections
CC   caused by prions, infections caused by bacteria, infections caused by
CC   fungi, ocular diseases, migraines, pain, sexual dysfunction, mood
CC   disorders, attention disorders, cognition disorders, hypotension,
CC   hypertension, psychotic disorders, dyskinesias, and organ transplant
CC   rejection. Kinase inhibitors are useful for treating diseases and
CC   disorders described above.
XX
SQ   Sequence 854 AA;

  Query Match           79.6%;  Score 4149;  DB 4;  Length 854;
  Best Local Similarity  91.8%;  Pred. No. 6.4e-316;
  Matches  827;  Conservative    4;  Mismatches   16;  Indels   54;  Gaps    2;

Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLCAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
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```
Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180

Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQV-------INMSL 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||           |:
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQCYAFRALRFLFSM 300

Qy        294 VLQYQVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 353
                  : : |   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ERNRPLFKRLFPTDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 360

Qy        354 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 420

Qy        414 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 480

Qy        474 RLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 533
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        481 RLWKIFIQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 540

Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
              ||||||||||||||||||||||||
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP-------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 -------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
              |
Db        854 P 854
```

RESULT 6
AAE39519
ID AAE39519 standard; protein; 854 AA.
XX
AC AAE39519;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human SGK237 protein.
XX
KW Human; 14815 protein; therapy; neurological disease; apoptotic disease;
KW metabolic disease; inflammatory disease; neuroprotective; cytostatic;
KW SGK237 protein.
XX
OS Homo sapiens.
XX
PN US2003134317-A1.
XX
PD 17-JUL-2003.
XX
PF 02-JAN-2003; 2003US-00335711.
XX
PR 02-JAN-2002; 2002US-0345853P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers RE;
XX
DR WPI; 2003-688693/65.
XX
PT New nucleic acid molecules, designated 14815 nucleic acids, useful for
PT preparing a composition for diagnosing or treating neurological,
PT inflammatory, apoptotic or metabolic diseases.
XX
PS Disclosure; Page 53-56; 59pp; English.
XX
CC The invention relates to novel 14815 protein, a member of kinase family
CC and polynucleotide encoding such protein. Sequences of the invention are
CC useful for detecting a molecule that binds to the polypeptide, including
CC molecules that modulate their activity. They are useful in the diagnosis
CC or treatment of neurological, inflammatory, apoptotic or metabolic
CC diseases. The present sequence is human SGK237 protein used in the
CC invention
XX
SQ Sequence 854 AA;

Query Match 79.6%; Score 4149; DB 7; Length 854;
Best Local Similarity 91.8%; Pred. No. 6.4e-316;
Matches 827; Conservative 4; Mismatches 16; Indels 54; Gaps 2;

```
Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLCAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60

Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180

Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQV-------INMSL 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||           |:
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQCYAFRALRFLFSM 300

Qy        294 VLQYQVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 353
                  : : |   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ERNRPLFKRLFPTDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 360

Qy        354 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 420

Qy        414 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 480

Qy        474 RLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 533
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        481 RLWKIFIQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 540
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```
Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
              |||||||||||||||||||||||||||
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
                              ||||||||||||||||||||||||||||||||||||||||||||||
Db        808 --------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
              |
Db        854 P 854
```

RESULT 7
ADN36596
ID ADN36596 standard; protein; 854 AA.
XX
AC ADN36596;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human protein kinase-like protein SGK237 protein sequence.
XX
KW cytostatic; antiasthmatic; antiparkinsonian; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; osteopathic;
KW immunosuppressive; cardiovascular; ophthalmological; cerebroprotective;
KW anticonvulsant; vasotropic; gene therapy; protein kinase; HPK3P23;
KW cancer; asthma; Parkinson's disease; inflammation; psoriasis;
KW rheumatoid arthritis; osteoporosis; graft-versus-host disease;
KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
KW epilepsy; ischemia; reperfusion.
XX
OS Homo sapiens.
XX
PN WO2004032877-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US032302.
XX
PR 10-OCT-2002; 2002US-0417209P.
XX
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
XX
PI Liu W, Wu L;
XX
DR WPI; 2004-340806/31.
DR N-PSDB; ADN36597.
XX
PT New human protein kinase, designated HPK3P23, and encoding
PT polynucleotides for diagnosing, preventing or treating kinase-related
PT diseases, such as cancer, Parkinson's disease, inflammation, stroke or
PT cardiovascular disorders.
XX
PS Example 2; SEQ ID NO 4; 210pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a protein kinase
CC designated HPK3P23 or a variant having at least 91% sequence identity.
CC The composition and methods are useful for diagnosing, prognosing,
CC preventing and treating kinase-related diseases, in particular, diseases
CC associated with aberrant expression of HPK3P23, such as cancer, asthma,
CC Parkinson's disease, inflammation, psoriasis, rheumatoid arthritis,
CC osteoporosis, graft-versus-host disease, cardiovascular disorders,
CC autoimmune disorders, retinal detachment, stroke, epilepsy or
CC ischemia/reperfusion. This sequence corresponds to the protein kinase-
CC like protein SGK237 protein and used in comparison with the HPK3P23
CC protein kinase of the invention.
XX
SQ Sequence 854 AA;

Query Match 79.6%; Score 4149; DB 8; Length 854;
Best Local Similarity 91.8%; Pred. No. 6.4e-316;
Matches 827; Conservative 4; Mismatches 16; Indels 54; Gaps 2;

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Qy          1 MRVLFDESVLPPTVYFKNCSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MRVLFDESVLPPTVYFKNCSILFLASLCAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQH 60

Qy         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAERL 120

Qy        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEIR 180

Qy        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQA 240

Qy        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQV-------INMSL 293
              |||||||||||||||||||||||||||||||||||||||||||||||          |:
Db        241 ACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQCYAFRALRFLFSM 300

Qy        294 VLQYQVIEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 353
                  : : |   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ERNRPLFKRLFPTDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQN 360

Qy        354 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KAPLKYIGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 420

Qy        414 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 NIVSELTIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEE 480

Qy        474 RLWKIFIQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 533
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 RLWKIFIQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSV 540

Qy        534 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VGTILYSCPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPV 600

Qy        594 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PEGIYSEKVTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERER 660

Qy        654 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RRTQRYFMEANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQ 720

Qy        714 ASYGKDEDRACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 773
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ASYGKDEDRACNEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILK 780

Qy        774 RSFSASGGERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQS 833
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                ||||||||||||||||||||||||||||
Db        781 RSFSASGGERQSQTRDFTGGTGSRPRP-------------------------------- 807

Qy        834 HSLPAVILRNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 893
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 --------------GPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLP 853

Qy        894 P 894
                |
Db        854 P 854


RESULT 8
ADA55439
ID   ADA55439 standard; protein; 484 AA.
XX
AC   ADA55439;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human protein, SEQ ID 3007.
XX
KW   Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW   Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW   inflammatory disease; osteoporosis; neurological disease.
XX
OS   Homo sapiens.
XX
PN   EP1293569-A2.
XX
PD   19-MAR-2003.
XX
PF   21-MAR-2002; 2002EP-00006586.
XX
PR   14-SEP-2001; 2001JP-00328381.
PR   24-JAN-2002; 2002US-0350435P.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-395539/38.
DR   N-PSDB; ADA53800.
XX
PT   New polynucleotides encoding full-length polypeptides, e.g. secretory
PT   and/or membrane proteins, useful for developing medicines for diseases in
PT   which the gene is involved, or as target molecules for gene therapy.
XX
PS   Claim 14; SEQ ID NO 3007; 205pp; English.
XX
CC   The present invention relates to novel human secretory or membrane
CC   proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC   ADA54071). The coding sequences are useful in the gene therapy of
CC   diseases caused by abnormalities of the proteins, e.g. cancer,
CC   inflammatory diseases, osteoporosis or neurological disease.
XX
SQ   Sequence 484 AA;

  Query Match             47.0%;  Score 2451;  DB 6;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-183;
  Matches  475;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        542 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 PEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKIVEAVYEPVPEGIYSEK 69

Qy        602 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VTDTISRCLTPDAEARPDIVEVSSMISDVMMKYLDNLSTSQLSLEKKLERERRRTQRYFM 129

Qy        662 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 EANRNTVTCHHELAVLSHETFEKASLSSSSSGAASLKSELSESADLPPEGFQASYGKDED 189

Qy        722 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 RACDEILSDDNFNLENAEKDTYSEVDDELDISDNSSSSSSSPLKESTFNILKRSFSASGG 249

Qy        782 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ERQSQTRDFTGGTGSRPRPALLPLDLLLKVPPHMLRAHIKEIEAELVTGWQSHSLPAVIL 309

Qy        842 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 RNLKDHGPQMGTFLWQASAGIAVSQRKVRQISDPIQQILIQLHKIIYITQLPPALHHNLK 369

Qy        902 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 RRVIERFKKSLFSQQSNPCNLKSEIKKLSQGSPEPIEPNFFTADYHLLHRSSGGNSLSPN 429

Qy        962 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 DPTGLPTSIELEEGITYEQMQTVIEEVLEESGYYNFTSNRYHSYPWGTKNHPTKR 484


RESULT 9
ADQ67014
ID   ADQ67014 standard; protein; 712 AA.
XX
AC   ADQ67014;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Novel human protein sequence #1987.
XX
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   gene therapy; diagnostic marker; morbid state; osteoporosis;
KW   neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   EP1440981-A2.
XX
PD   28-JUL-2004.
XX
PF   21-JAN-2004; 2004EP-00001196.
XX
PR   21-JAN-2003; 2003JP-00102206.
PR   09-MAY-2003; 2003JP-00131392.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Nagai K,  Irie R;
XX
DR   WPI; 2004-535376/52.
DR   N-PSDB; ADQ64826.
XX
PT   Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT   Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS   Claim 1; SEQ ID NO 4175; 2449pp; English.
XX
CC   The invention relates to 2495 novel polynucleotides (I) and their encoded
CC   polypeptides, sequences hybridizing to these nucleotides, sequences
CC   encoding partial polypeptides and sequences having 70% or 90% identity to
CC   the nucleotide and protein sequences. The nucleotides and polypeptides
CC   are useful as diagnostic markers or therapeutic target for the diseases
CC   or morbid states. They are also useful for treating osteoporosis,
CC   neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC   dementia and various cancers. This sequence corresponds to a protein
CC   sequence of the invention.
```

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XX
SQ   Sequence 712 AA;

  Query Match           46.3%;  Score 2413;  DB 8;  Length 712;
  Best Local Similarity  84.2%;  Pred. No. 8e-180;
  Matches  490;  Conservative    9;  Mismatches   27;  Indels   56;  Gaps    4;

Qy         12 PTVYFKN----------CSILFLASLGAFGVLTGLLVWSFMQYMEIVANEYLGYGEEQ 59
              |:::|              |    | |||         : :  ||||||||||||||||
Db        128 PSIHFLRVLICLRLLMRDPCYQEILHSLGG--------IENLAQYMEIVANEYLGYGEEQ 179

Qy         60 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAE- 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 HTVDKLVNMTYIFQKLAAVKDQREWVTTSGAHKTLVNLLGARDTNVLLGSLLALASLAES 239

Qy        119 ----------------------------RLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 150
                                         ||||||||||||||||||||||||||||||||
Db        240 QECREKISELNIVENLLMILHEYDLLSKRLTAELLRLLCAEPQVKEQVKLYEGIPVLLSL 299

Qy        151 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LHSDHLKLLWSIVWILVQVCEDPETSVEIRIWGGIKQLLHILQGDRNFVSDHSSIGSLSS 359

Qy        211 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ANAAGRIQQLHLSEDLSPREIQENTFSLQAACCAALTELVLNDTNAHQVVQENGVYTIAK 419

Qy        271 LILPNKQKNAAKSNLLQV-------INMSLVLQYQVIEILGNYDLFEIFIDIGHYVRDIS 323
              ||||||||||||||||||          |:    : : |   ||||||||||||||||
Db        420 LILPNKQKNAAKSNLLQCYAFRALRFLFSMERNRPLFKRLFPTDLFEIFIDIGHYVRDIS 479

Qy        324 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKVRKH 539

Qy        384 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 SGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLENDR 599

Qy        444 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 LYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDLTPN 659

Qy        504 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCPEVL 545
              |||||||||||||||||||||||||||||||||| : |
Db        660 NIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYSCVQHL 701


RESULT 10
AAU17282
ID   AAU17282 standard; protein; 229 AA.
XX
AC   AAU17282;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Novel signal transduction pathway protein, Seq ID 847.
XX
KW   Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW   antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW   immune system disorder; rheumatoid arthritis; inflammatory condition;
KW   organ transplant rejection; infection; hepatitis C; blood disorder;
KW   sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW   cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW   reproductive system; gastrointestinal; liver disorder; AIDS;
KW   acquired immune deficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200154733-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001312.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
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PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
PR   08-NOV-2000; 2000US-0246476P.
PR   08-NOV-2000; 2000US-0246477P.
PR   08-NOV-2000; 2000US-0246478P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
PR   17-NOV-2000; 2000US-0249208P.
PR   17-NOV-2000; 2000US-0249209P.
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PR   17-NOV-2000; 2000US-0249265P.
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PR   01-DEC-2000; 2000US-0250160P.
PR   01-DEC-2000; 2000US-0250391P.
PR   05-DEC-2000; 2000US-0251030P.
PR   05-DEC-2000; 2000US-0251988P.
PR   05-DEC-2000; 2000US-0256719P.
PR   06-DEC-2000; 2000US-0251479P.
PR   08-DEC-2000; 2000US-0251856P.
PR   08-DEC-2000; 2000US-0251868P.
PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465460/50.
DR   N-PSDB; AAS27199.
XX
PT   Novel polypeptides useful for diagnosing, treating, preventing and/or
PT   prognosing disorders related to the proteins, including cancers, immune
PT   disorders and neuronal disorders.
XX
PS   Claim 1; SEQ ID NO 847; 880pp; English.
XX
CC   The invention relates to novel isolated polypeptides (I), and
CC   polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC   diagnosing, preventing and treating diseases including immune system
CC   disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC   disorders (e.g rheumatoid arthritis), inflammatory conditions, organ
CC   transplant rejections and graft versus host disease, infectious diseases
CC   (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC   other blood-related disorders (sickle cell anaemia), myeloproliferative
CC   disorders, primary haematopoietic disorders, hyperproliferative disorders
CC   (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC   Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC   (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC   glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC   respiratory disorders, dermatological disorders, in wound healing,
CC   epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC   disease), reproductive system disorders, gastrointestinal disorder
CC   (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC   B-cell responsiveness to pathogens, activators of T-cells, to induce
CC   higher affinity antibodies, and as a means to induce tumour proliferation
CC   in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC   AAU17683 represent novel signal transduction pathway protein, amino acid
CC   sequences of the invention
XX

  Query Match             22.5%;  Score 1172;  DB 4;  Length 229;
  Best Local Similarity   99.1%;  Pred. No. 3.1e-83;
  Matches  227;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        312 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGS 371
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Qy        432 VRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHK 491
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Db        121 VRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHK 180

Qy        492 EKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
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Db        181 EKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 229


RESULT 11
ADB93990
ID   ADB93990 standard; protein; 229 AA.
XX
AC   ADB93990;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human novel protein #224.
XX
KW   human; autoimmune disease; Parkinson's disease; silicosis;
KW   gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW   immunosuppressive agent; adjuvant; enhance immune response;
KW   higher affinity antibody induction;
KW   increased serum immunoglobulin concentration.
XX
OS   Homo sapiens.
XX
PN   US2002168711-A1.
XX
```

PD 14-NOV-2002.
XX
PF 17-JAN-2001; 2001US-00764868.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
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PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
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PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241809P.
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PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-719985/68.
DR N-PSDB; ADB93367.
XX
PT New isolated polypeptide useful for diagnosing and treating
PT immunosuppressive conditions such as autoimmune disease and Parkinson's
PT disease.
XX
PS Claim 11; SEQ ID NO 847; 345pp; English.
XX
CC The invention relates to an isolated polypeptide. The polypeptide is
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in The nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents the amino acid sequence of a novel human
CC protein. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format direct from
CC USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.
XX
SQ Sequence 229 AA;

Query Match 22.5%; Score 1172; DB 7; Length 229;
Best Local Similarity 99.1%; Pred. No. 3.1e-83;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGS 60

Qy        372 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNI 431
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Db         61 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPXI 120

Qy        432 VRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHK 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHK 180

Qy        492 EKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 229
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RESULT 12
AAU87169
ID AAU87169 standard; protein; 223 AA.
XX
AC AAU87169;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #79.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.

```
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001332.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
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PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
```

DR WPI; 2001-581633/65.
DR N-PSDB; ABK43499.
XX
PT New isolated nucleic acid encoding a protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as food additives or
PT preservatives.
XX
PS Claim 9; SEQ ID NO 687; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (III) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amylotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 21.7%; Score 1129; DB 4; Length 223;
Best Local Similarity 99.5%; Pred. No. 7e-80;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        321 DISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKV 380
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Db          4 DISAYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKV 63

Qy        381 RKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLE 440
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Db         64 RKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLE 123

Qy        441 NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDL 500
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Db        124 NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDL 183

Qy        501 TPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
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Db        184 TPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 223
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RESULT 13
ADI54484
ID ADI54484 standard; protein; 223 AA.
XX
AC ADI54484;
XX
DT 22-APR-2004 (first entry)
XX
DE Novel human protein seq id 687.
XX
KW neuroprotective; nootropic; antiparkinsonian; anticonvulsant;
KW antidiabetic; antirheumatic; antiarthritic; dermatological;
KW antiinflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;
KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;
KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
KW cardiovascular-; antiarteriosclerotic; antiarrhythmic; cardiant;
KW nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;
KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
KW amyotrophic lateral sclerosis; multiple sclerosis;
KW immune system disorder; diabetes; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;
KW inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; infectious disease;
KW HIV infection; hepatitis infection; bacterial infection;
KW fungal infection; parasitic infection; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;
KW renal disorder; acute glomerulonephritis; pyelonephritis;
KW renal lithiasis; proliferative disorder; cancerous diseases; human.
XX
OS Homo sapiens.
XX
PN US2004018969-A1.
XX
PD 29-JAN-2004.
XX
PF 17-JAN-2001; 2001US-00764875.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
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PR 23-AUG-2000; 2000US-0227009P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 08-DEC-2000; 2000US-0251869P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2004-122079/12.
DR N-PSDB; ADI53886.
XX
PT New polypeptides and nucleic acid molecules, useful for detecting,
PT preventing, diagnosing, prognosticating, treating or ameliorating medical
PT conditions e.g. neural disorders, reproductive disorders or infectious
PT diseases.
XX
PS Claim 11; SEQ ID NO 687; 413pp; English.
XX
CC The invention describes an isolated polypeptide comprising an amino acid
CC sequence at least 90% identical to: a polypeptide fragment, domain,
CC epitope, or full-length protein of any one of 607 amino acid sequences
CC (I) described in the specification; a polypeptide fragment of (I), or the
CC encoded sequence contained in (II), having biological activity; or a
CC variant, allelic variant, or a species homologue of (I). The polypeptides
CC and nucleic acid molecules are useful for detecting, preventing,
CC diagnosing, prognosticating, treating or ameliorating medical conditions
CC such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease,
CC Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,
CC immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic

Query Match 21.7%; Score 1129; DB 8; Length 223;
Best Local Similarity 99.5%; Pred. No. 7e-80;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        321 DISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGSGAFGCVYKV 380
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db          4 DISAYEELVSKLNLLVEDELKQIAENIESINQNKAPSKYIGNYAILDHLGSGAFGCVYKV 63

Qy        381 RKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLE 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 RKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSELTIIKEQLYHPNIVRYYKTFLE 123

Qy        441 NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDL 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 NDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIFIQLCLALRYLHKEKRIVHRDL 183

Qy        501 TPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 540
              |||||||||||||||||||||||||||||||||||||||
Db        184 TPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILYS 223
```

RESULT 14
AAU96909
ID AAU96909 standard; protein; 261 AA.
XX
AC AAU96909;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human serine threonine kinase protein.
XX
KW Human; serine threonine kinase; enzyme; cancer; leukaemia; inflammation;
KW lymphoma; melanoma; CNS disorder; Parkinson's disease; stroke; COPD;
KW traumatic brain injury; diabetes; eating disorder; obesity; anorexia;
KW cachexia; allergy; anaphylaxis; asthma;

```
KW   chronic obstructive pulmonary disease.
XX
OS   Homo sapiens.
XX
PN   WO200233095-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-EP011893.
XX
PR   16-OCT-2000; 2000US-0240067P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Smolyar A;
XX
DR   WPI; 2002-435537/46.
DR   N-PSDB; ABK52073.
XX
PT   New human serine-threonine protein kinase and encoding polynucleotides,
PT   useful for diagnosing, treating and preventing central nervous system
PT   disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS   Claim 1; Fig 2; 98pp; English.
XX
CC   This invention relates to the DNA and protein sequences of a novel human
CC   serine-threonine protein kinase (STPK). The STPK polypeptide and the
CC   polynucleotide encoding the STPK polypeptide are useful in the diagnosis,
CC   treatment and prevention of cancers (e.g. leukaemia, lymphoma or
CC   melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or traumatic
CC   brain injury), diabetes, eating disorders (e.g. obesity, anorexia, or
CC   cachexia), allergies, anaphylaxis, asthma, inflammation, chronic
CC   obstructive pulmonary disease (COPD). Human STPK may also be used to
CC   identify compounds which may act as activators or inhibitors at the
CC   enzyme's active site, to raise specific antibodies which can block the
CC   enzyme and effectively reduce its activity or to identify other proteins
CC   which bind to or interact with the STPK polypeptide and modulate its
CC   activity. The proteins can be used to immunise a mammal to produce
CC   polyclonal antibodies, and in diagnostic assays for detecting diseases
CC   and abnormalities or susceptibility to diseases and abnormalities related
CC   to the presence of mutations in the nucleic acids encoding the enzymes.
CC   The expression vector comprising nucleotide sequence and the reagent
CC   which modulates the activity of STPK are useful in preparing a medicament
CC   for modulating the activity of an STPK in a disease, such as cancer, a
CC   CNS disorder, diabetes, asthma, or COPD. The present sequence represents
CC   the human serine threonine kinase protein of the invention
XX
SQ   Sequence 261 AA;

  Query Match             18.8%;  Score 980.5;  DB 5;  Length 261;
  Best Local Similarity   45.0%;  Pred. No. 4e-68;
  Matches  224;  Conservative    7;  Mismatches   20;  Indels  247;  Gaps    5;

Qy        120 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETSVEI 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db          1 LTAELLRLLCAEPQVKEQVKLYEGIPVLLSLLHSDHLKLLWSIVWILVQVCEDPETTVEI 60

Qy        180 RIWGGIKQLLHILQGDRNFVSDHSSIGSLSSANAAGRIQQLHLSEDLSPREIQENTFSLQ 239
              ||||||||||||||   |
Db         61 RIWGGIKQLLHILQGSVTF---------------------------------------- 79

Qy        240 AACCAALTELVLNDTNAHQVVQENGVYTIAKLILPNKQKNAAKSNLLQVINMSLVLQYQV 299
                |
Db         80 ---C------------------------------------------------------- 80

Qy        300 IEILGNYDLFEIFIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKY 359
                       :|:||
Db         81 ----------DIYID---------------------------------------- 85

Qy        360 IGNYAILDHLGSGAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVRNIVSEL 419

Db         86 ------------------------------------------------------------ 85

Qy        420 TIIKEQLYHPNIVRYYKTFLENDRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 479
                                                ||||||||||||||||||||||||||||||
Db         86 ----------------------DRLYIVMELIEGAPLGEHFSSLKEKHHHFTEERLWKIF 123

Qy        480 IQLCLALRYLHKEKRIVHRDLTPNNIMLGDKDKVTVTDFGLAKQKQENSKLTSVVGTILY 539
              |||||||||||||||||| |||||||||||||: ||  :|     | :    ||
Db        124 IQLCLALRYLHKEKRIVHRDQTPNNIMLGDKDKVTVSSFGDLQQMGVEIMLRNTSQHILP 183

Qy        540 S---CPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKI-------VEAV 589
              |    ||||||||||||||||||||||||||||||||||||||||||:       ||||
Db        184 SQKIFPEVLKSEPYGEKADVWAVGCILYQMATLSPPFYSTNMLSLATKVSNAGRQKVEAV 243

Qy        590 YEPVPEGIYSEKVTDTIS 607
              ||||||||||||||||||
Db        244 YEPVPEGIYSEKVTDTIS 261


RESULT 15
AAU17603
ID   AAU17603 standard; protein; 106 AA.
XX
AC   AAU17603;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Novel signal transduction pathway protein, Seq ID 1168.
XX
KW   Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW   antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW   immune system disorder; rheumatoid arthritis; inflammatory condition;
KW   organ transplant rejection; infection; hepatitis C; blood disorder;
KW   sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW   cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW   reproductive system; gastrointestinal; liver disorder; AIDS;
KW   acquired immune deficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200154733-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001312.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
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PR   14-AUG-2000; 2000US-0224519P.
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PR   14-AUG-2000; 2000US-0225214P.
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PR 13-OCT-2000; 2000US-0239937P.
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PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241809P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246610P.
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PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
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PR 17-NOV-2000; 2000US-0249217P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDB; AAS27520.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 1168; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX

Query Match 10.0%; Score 520; DB 4; Length 106;
Best Local Similarity 99.0%; Pred. No. 1.3e-32;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        312 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPLKYIGNYAILDHLGS 371
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 FIDIGHYVRDISAYEELVSKLNLLVEDELKQIAENIESINQNKAPXKYIGNYAILDHLGS 60

Qy        372 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 413
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 GAFGCVYKVRKHSGQNLLAMKEVNLHNPAFGKDKKDRDSSVR 102
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